

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:29:28 ; Search time 53 Seconds  
(without alignments)  
613.075 Million cell updates/sec

Title: US-09-620-955b-2

Perfect score: 115

Sequence: 1 QVQLQESGGLVQPGSLRL.....CARDYFDLWGRGIVTVSS 115

Scoring table: Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 934974

Minimum DB seq length: 0

Maximum DB seq length: 115

Post-processing: Listing first 100 summaries

Database : A: Genesep29Jan04:\*

- 1: Genesep1980s:\*
- 2: Genesep1990s:\*
- 3: Genesep2000s:\*
- 4: Genesep2001s:\*
- 5: Genesep2002s:\*
- 6: Genesep2003as:\*
- 7: Genesep2003bs:\*
- 8: Genesep2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	115	100.0	115	4	AAB69601 Huntingti
2	65	56.5	115	5	AAW51164 Anti-tumo
3	63	54.8	98	3	AAB40116 Anti-hill
4	63	54.8	98	3	AAB40104 Anti-hill
5	63	54.8	98	3	AAB40118 Anti-hill
6	63	54.8	98	3	AAB40115 Anti-hill
7	63	54.8	98	3	AAB40120 Anti-hill
8	63	54.8	98	3	AAB40105 Anti-hill
9	63	54.8	98	3	AAB40106 Anti-hill
10	63	54.8	98	3	AAB40102 Anti-hill
11	63	54.8	98	3	AAB40101 Anti-hill
12	63	54.8	98	3	AAB40110 Anti-hill
13	63	54.8	98	3	AAB40117 Anti-hill
14	63	54.8	98	3	AAB40128 Anti-hill
15	63	54.8	98	3	AAB40099 Anti-hill
16	63	54.8	98	3	AAB40103 Anti-hill
17	63	54.8	98	4	AAW67512 Heavy cha
18	63	54.8	98	4	AAW67507 Light cha
19	63	54.8	98	5	ABG78201 Human Fv
20	63	54.8	98	5	ABG78199 Human Fv
21	63	54.8	98	5	ABG78200 Human Fv
22	63	54.8	98	5	ABG78190 Human ant
23	63	54.8	98	5	ABG91891 Human ant
24	63	54.8	98	5	ABG91892 Human ant
25	63	54.8	98	6	ABO27091 Human ger

26	63	54.8	98	7	ADC99832 Germline
27	63	54.8	98	7	ADC99833 Anti-huma
28	63	54.8	98	7	ADD05436 Anti-MUC1
29	63	54.8	98	7	ADD05437 Anti-MUC1
30	63	54.8	113	4	AAU02538 Anti-adip
31	63	54.8	113	4	AAU02537 Anti-adip
32	62	53.9	98	3	AAU02537 Anti-adip
33	62	53.9	98	3	AAU02537 Anti-adip
34	62	53.9	98	3	AAU02537 Anti-adip
35	62	53.9	98	3	AAU02537 Anti-adip
36	62	53.9	98	5	ABG78205 Human Fv
37	62	53.9	98	5	ABG78205 Human Fv
38	62	53.9	98	5	ABG78205 Human Fv
39	62	53.9	98	5	ABG78205 Human Fv
40	62	53.9	98	5	ABG78205 Human Fv
41	62	53.9	98	5	ABG78205 Human Fv
42	62	53.9	98	5	ABG78205 Human Fv
43	58	50.4	95	3	ABG78205 Human Fv
44	54	47.0	94	3	ABG78205 Human Fv
45	52	45.2	98	3	ABG78205 Human Fv
46	48	41.7	98	3	ABG78205 Human Fv
47	48	41.7	98	3	ABG78205 Human Fv
48	46	40.0	89	6	ABG78205 Human Fv
49	46	40.0	89	6	ABG78205 Human Fv
50	46	40.0	89	6	ABG78205 Human Fv
51	46	40.0	89	6	ABG78205 Human Fv
52	46	40.0	89	6	ABG78205 Human Fv
53	46	40.0	89	6	ABG78205 Human Fv
54	46	40.0	89	6	ABG78205 Human Fv
55	46	40.0	89	6	ABG78205 Human Fv
56	46	40.0	89	6	ABG78205 Human Fv
57	46	40.0	89	6	ABG78205 Human Fv
58	46	40.0	89	6	ABG78205 Human Fv
59	45	39.1	98	3	ABG78205 Human Fv
60	45	39.1	98	3	ABG78205 Human Fv
61	44	38.3	115	3	ABG78205 Human Fv
62	44	38.3	115	3	ABG78205 Human Fv
63	44	38.3	115	3	ABG78205 Human Fv
64	44	38.3	115	3	ABG78205 Human Fv
65	42	36.5	98	3	ABG78205 Human Fv
66	41	35.7	98	4	ABG78205 Human Fv
67	41	35.7	98	4	ABG78205 Human Fv
68	41	35.7	98	4	ABG78205 Human Fv
69	41	35.7	98	4	ABG78205 Human Fv
70	41	35.7	98	4	ABG78205 Human Fv
71	40	34.8	95	2	ABG78205 Human Fv
72	40	34.8	95	2	ABG78205 Human Fv
73	40	34.8	95	2	ABG78205 Human Fv
74	40	34.8	95	2	ABG78205 Human Fv
75	40	34.8	95	2	ABG78205 Human Fv
76	40	34.8	95	2	ABG78205 Human Fv
77	40	34.8	95	2	ABG78205 Human Fv
78	40	34.8	95	2	ABG78205 Human Fv
79	40	34.8	95	2	ABG78205 Human Fv
80	40	34.8	95	2	ABG78205 Human Fv
81	40	34.8	95	2	ABG78205 Human Fv
82	40	34.8	95	2	ABG78205 Human Fv
83	40	34.8	95	2	ABG78205 Human Fv
84	40	34.8	95	2	ABG78205 Human Fv
85	40	34.8	95	2	ABG78205 Human Fv
86	40	34.8	95	2	ABG78205 Human Fv
87	39	33.9	98	3	ABG78205 Human Fv
88	39	33.9	98	3	ABG78205 Human Fv
89	39	33.9	98	3	ABG78205 Human Fv
90	39	33.9	98	3	ABG78205 Human Fv
91	39	33.9	98	3	ABG78205 Human Fv
92	39	33.9	98	3	ABG78205 Human Fv
93	39	33.9	98	3	ABG78205 Human Fv
94	39	33.9	98	3	ABG78205 Human Fv
95	39	33.9	98	3	ABG78205 Human Fv
96	39	33.9	98	3	ABG78205 Human Fv
97	39	33.9	98	3	ABG78205 Human Fv
98	39	33.9	98	3	ABG78205 Human Fv

99 39 33.9 109 7 ADC60990 Human ant  
100 39 33.9 112 2 AAR12274 Anti-huma

## ALIGNMENTS

RESULT 1  
AAB69601  
ID AAB69601 standard; protein; 115 AA.  
AC AAB69601;  
XX  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Huntingtin minimal svf binding region #1.  
XX  
KW Neurological disorder; Huntington's disease; Alzheimer's disease;  
KW Parkinson's disease; prion disease; frontotemporal dementia;  
KW amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy;  
KW dentatorubral-pallidoluysian atrophy; spinocerebellar ataxia type 1, SCA2;  
KW SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabody.  
XX  
OS Unidentified.  
XX  
XX WO200106989-A2.  
XX  
XX PD 01-FEB-2001.  
XX  
XX PF 24-JUL-2000; 2000WO-US020131.  
XX  
XX PR 27-JUL-1999; 99US-0146047P.  
XX  
XX PR 21-JUL-2000; 2000US-00620955.  
XX  
XX PA (HUST/) HUSTON J S.  
XX  
XX PA (MESS/) MESSER A.  
XX  
XX PA (LECE/) LECERF J.  
XX  
XX PI Huston JS, Messer A, Lecerf J;  
XX  
XX DR WPI; 2001-192700/19.  
XX  
XX DR N-PSDB; AAF58705.  
XX  
XX PT Inhibiting intracellular polypeptide accumulation, useful for treating  
XX neurological disorders, e.g. Alzheimer's disease, comprises contacting  
XX the polypeptide with a specific intrabody.  
XX  
XX PS Claim 21; Page 93; 108pp; English.  
XX  
XX CC The present invention describes a method for inhibiting the formation of  
XX aggregates of certain proteins, involving contacting the protein with a  
XX binding molecule known as an intrabody. Proteins to be bound include  
XX those associated with neurological disorders, and so the method can be  
XX used in the prevention of diseases such as Alzheimer's, Parkinson's and  
XX Huntington's diseases, prion disease, frontotemporal dementia,  
XX amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy,  
XX dentatorubal-pallidoluysian atrophy, spinocerebellar ataxia type 1  
XX (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7  
XX  
XX SQ Sequence 115 AA;

Query Match 100.0%; Score 115; DB 4; Length 115;  
Best Local Similarity 100.0%; Pred. No. 6.9e-104;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QVQLQESGGGLVPGGSLRLSCAASGFTFSYSMSVWRQAPGKLEWVAIVSDGSKYY 60  
Db 1 QVQLQESGGGLVPGGSLRLSCAASGFTFSYSMSVWRQAPGKLEWVAIVSDGSKYY 60  
Qy 61 ADSVKGRFTTSDNSKNTLYLQMSLRAEDTAVYYCARDRYFDLWGRGLTVTSS 115  
Db 61 ADSVKGRFTTSDNSKNTLYLQMSLRAEDTAVYYCARDRYFDLWGRGLTVTSS 115

RESULT 2  
AAM51164

ID AAM51164 standard; protein; 115 AA.

AC AAM51164;

DT 10-JUN-2002 (first entry)

DE Anti-tumour necrosis factor antibody heavy chain variable region.

XX  
XX KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
KW complementarity determining region; antirheumatic; antiarthritic;  
KW antiulcer; antiasthmatic; anti-allergic; antinflammatory; antisticking;  
KW antidiabetic; antiatherosclerotic; antiatherosclerotic; vasotropic;  
KW antiangiinal; cardiac; antibacterial; virucide; fungicide; antileptotic;  
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;  
KW human; diagnosis; therapy.

OS Homo sapiens.

XX  
XX PH Location/Qualifiers

FT Region 1..30

FT /label= FR1

FT Region 31..35

FT /label= CDR1

FT Region 36..49

FT /label= FR2

FT Region 50..66

FT /label= CDR2

FT Region 67..98

FT /label= FR3

FT Region 99..107

FT /label= CDR3

FT Region 108..115

FT /label= J6

XX WO200212502-A2.

XX  
XX PD 14-FEB-2002.

XX  
XX PF 07-AUG-2001; 2001WO-US024785.

XX  
XX PR 07-AUG-2000; 2000US-0223360P.

XX  
XX PR 29-SEP-2000; 2000US-0236826P.

XX  
XX PR 01-AUG-2001; 2001US-00920137.

XX  
XX PA (CENZ ) CENTOCOR INC.

XX  
XX PI Giles-Komar J, Knight DM, Heavner G, Scallan B, Shealy D;

XX  
XX WPI; 2002-217194/27.

XX  
XX DR Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
XX treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
XX angina pectoris, myocardial infarction, leprosy.

XX  
XX PS Claim 9; Page 129; 131pp; English.

XX  
XX CC The present sequence is that of the heavy chain variable region of an  
XX anti-tumour necrosis factor (TNF) antibody of the invention. The  
XX invention provides isolated human, primate, rodent, mammalian, chimeric,  
XX humanised and/or complementarity determining region (CDR)-grafted anti-  
XX TNF antibodies, immunoglobulins, cleavage products and other specified  
XX portions and variants, as well as anti-TNF antibody compositions,  
XX encoding or complementary nucleic acids, vectors, host cells,  
XX compositions, formulations, devices, transgenic animals, transgenic  
XX plants, and methods of making and using them. The anti-TNF antibody  
XX comprises at least a portion of an immunoglobulin molecule, especially  
XX the heavy chain and/or light chain variable regions given in the present  
XX sequence and in AAM51165, or either all of the CDRs of the heavy chain  
XX (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
XX 63). The antibody may inhibit TNF-induced cell adhesion molecules.

CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
 CC in a mouse model. It is useful for diagnosing or treating a TNF related  
 CC condition in a cell, tissue, organ or animal (claimed) such as rheumatoid  
 CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,  
 CC sickle cell anemia, diabetes, a cardiovascular disease such as  
 CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
 CC myocardial infarction, an infectious disease in a cell such as bacterial,  
 CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
 CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
 CC Creutzfeldt-Jakob disease  
 CC  
 SQ Sequence 115 AA;  
 Query Match 56.5%; Score 65; DB 5; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-55;  
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WVRQAPGKLEWVAVISYDGSNKYVADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95  
 DB 36 WVRQAPGKLEWVAVISYDGSNKYVADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95  
 QY 96 CARDR 100  
 DB 96 CARDR 100  
 RESULT 3  
 AAB40116  
 ID AAB40116 standard; protein; 98 AA.  
 XX  
 AC AAB40116;  
 XX  
 DT 05-FEB-2001 (first entry)  
 XX  
 DE Anti-hll12 antibody H chain V region amino acid sequence SEQ ID 642.  
 XX  
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200056772-A1.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US007946.  
 XX  
 PR 25-MAR-1999; 99US-0126603P.  
 XX  
 PA (BADI ) BASF AG.  
 XX (GEMY ) GENETICS INST INC.  
 XX  
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX  
 DR WPI; 2000-638250/61.  
 XX  
 PT New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 XX  
 PS Claim 75; Page 122; 377pp; English.  
 XX  
 CC This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39495-B39516 represent human

CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
 CC C61071. The antibody of the invention is a neutralising antibody and has  
 CC antirheumatic; antiarthritic; antisclerotic; antiasthmatic; antiparasitic;  
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease,  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 CC disorders  
 CC  
 SQ Sequence 98 AA;  
 Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WVRQAPGKLEWVAVISYDGSNKYVADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95  
 DB 36 WVRQAPGKLEWVAVISYDGSNKYVADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95  
 QY 96 CAR 98  
 DB 96 CAR 98  
 RESULT 4  
 AAB40104  
 ID AAB40104 standard; protein; 98 AA.  
 XX  
 AC AAB40104;  
 XX  
 DT 05-FEB-2001 (first entry)  
 XX  
 DE Anti-hll12 antibody H chain V region amino acid sequence SEQ ID 630.  
 XX  
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200056772-A1.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US007946.  
 XX  
 PR 25-MAR-1999; 99US-0126603P.  
 XX  
 PA (BADI ) BASF AG.  
 XX (GEMY ) GENETICS INST INC.  
 XX  
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX  
 DR WPI; 2000-638250/61.  
 XX  
 PT New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 XX

PS Claim 75; Page 121; 377pp; English.

XX This invention relates to a new human antibody specific for human interleukin-12 (IL-12). The invention also includes antigen binding portions that bind to IL-12. Sequences AAB39485-B39516 represent human anti-IL-12 antibody heavy and light chain complementarity determining region (CDR) amino acid sequences, and also includes variable region amino acid sequences. Other variable region amino acid sequences are given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771 represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063 represent other CDR sequences. Light chain CDR3 consensus sequences are given in AAB40064-B40067. Primers used in the identification and construction of the antibodies of the invention are given in AAC61062-C61071. The antibody of the invention is a neutralising antibody and has antirheumatic; antiarthritic; antisclerotic; antiinflammatory; antineuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic; antibacterial and immunosuppressive activity. The antibodies or antigen binding fragments are useful in the treatment of disorders associated with detrimental release of human IL-12, especially Crohn's disease, multiple sclerosis and rheumatoid arthritis. They can also be used in the manufacture of a pharmaceutical composition to treat human IL-12 disorders

XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95  
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95  
QY 96 CAR 98  
DB 96 CAR 98

RESULT 5  
AAB40118  
ID AAB40118 standard; protein; 98 AA.  
AC AAB40118;  
XX  
XX 05-FEB-2001 (first entry)  
XX Anti-hil12 antibody H chain V region amino acid sequence SEQ ID 644.  
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
KW multiple sclerosis; rheumatoid arthritis.  
XX Homo sapiens.  
XX WO200056772-A1.  
XX 28-SEP-2000.  
XX 24-MAR-2000; 2000WO-US007946.  
XX 25-MAR-1999; 99US-0126603P.  
XX (BADI ) BASF AG.  
XX (GENY ) GENETICS INST INC.  
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Wyles A;  
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to treat disorders characterized by aberrant IL-12 expression e.g. Crohn's disease and multiple sclerosis.

XX Claim 75; Page 122; 377pp; English.

XX This invention relates to a new human antibody specific for human interleukin-12 (IL-12). The invention also includes antigen binding portions that bind to IL-12. Sequences AAB39485-B39516 represent human anti-IL-12 antibody heavy and light chain complementarity determining region (CDR) amino acid sequences, and also includes variable region amino acid sequences. Other variable region amino acid sequences are given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771 represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063 represent other CDR sequences. Light chain CDR3 consensus sequences are given in AAB40064-B40067. Primers used in the identification and construction of the antibodies of the invention are given in AAC61062-C61071. The antibody of the invention is a neutralising antibody and has antirheumatic; antiarthritic; antisclerotic; antiinflammatory; antineuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic; antibacterial and immunosuppressive activity. The antibodies or antigen binding fragments are useful in the treatment of disorders associated with detrimental release of human IL-12, especially Crohn's disease, multiple sclerosis and rheumatoid arthritis. They can also be used in the manufacture of a pharmaceutical composition to treat human IL-12 disorders

XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95  
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95  
QY 96 CAR 98  
DB 96 CAR 98

RESULT 6  
AAB40115  
ID AAB40115 standard; protein; 98 AA.  
AC AAB40115;  
XX  
XX 05-FEB-2001 (first entry)  
XX Anti-hil12 antibody H chain V region amino acid sequence SEQ ID 641.  
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
KW multiple sclerosis; rheumatoid arthritis.  
XX Homo sapiens.  
XX WO200056772-A1.  
XX 28-SEP-2000.  
XX 24-MAR-2000; 2000WO-US007946.  
XX 25-MAR-1999; 99US-0126603P.  
XX (BADI ) BASF AG.  
XX (GENY ) GENETICS INST INC.  
XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;

PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX WPI; 2000-638250/61.  
 XX New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 XX Claim 75; Page 122; 377pp; English.  
 XX This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
 CC C61071. The antibody of the invention is a neutralising antibody and has  
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;  
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease,  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 CC disorders  
 XX Sequence 98 AA;  
 SQ Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95  
 Db |||||  
 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95  
 QY 96 CAR 98  
 Db |||||  
 96 CAR 98  
 RESULT 7  
 AAB40120  
 ID AAB40120 standard; protein; 98 AA.  
 AC AAB40120;  
 XX 05-FEB-2001 (first entry)  
 XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 646.  
 XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 XX complementarity determining region; CDR; antirheumatic; antiarthritic;  
 XX antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 XX multiple sclerosis; rheumatoid arthritis.  
 XX Homo sapiens.  
 OS WO200056772-A1.  
 XX 28-SEP-2000.  
 XX 24-MAR-2000; 2000WO-US007946.  
 XX 25-MAR-1999; 99US-0126603P.

XX (BADI ) BASF AG.  
 PA (GEMY ) GENETICS INST INC.  
 XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX WPI; 2000-638250/61.  
 XX New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 XX Claim 75; Page 122; 377pp; English.  
 XX This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
 CC C61071. The antibody of the invention is a neutralising antibody and has  
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;  
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease,  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 CC disorders  
 XX Sequence 98 AA;  
 SQ Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95  
 Db |||||  
 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYY 95  
 QY 96 CAR 98  
 Db |||||  
 96 CAR 98  
 RESULT 8  
 AAB40105  
 ID AAB40105 standard; protein; 98 AA.  
 XX AAB40105;  
 XX 05-FEB-2001 (first entry)  
 XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 631.  
 XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 XX complementarity determining region; CDR; antirheumatic; antiarthritic;  
 XX antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 XX multiple sclerosis; rheumatoid arthritis.  
 XX Homo sapiens.  
 OS WO200056772-A1.  
 XX 25-MAR-1999; 99US-0126603P.

PD 28-SEP-2000.  
 XX  
 XX  
 XX 24-MAR-2000; 2000WO-US007945.  
 XX  
 XX 25-MAR-1999; 99US-0126603P.  
 XX  
 XX (BADI ) BASF AG.  
 XX (GEMY ) GENETICS INST INC.  
 XX  
 XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX  
 XX WPI; 2000-638250/61.  
 XX  
 XX New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 XX  
 XX Claim 75; Page 121; 377pp; English.  
 XX  
 XX This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
 CC C61071. The antibody of the invention is a neutralising antibody and has  
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;  
 CC neuroprotective; antipapillary; antiasthmatic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease,  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 XX disorders  
 XX  
 XX Sequence 98 AA;  
 SQ  
 Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRADTVAVY 95  
 DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRADTVAVY 95  
 QY 96 CAR 98  
 DB 96 CAR 98  
 RESULT 9  
 AAB40106  
 ID AAB40106 standard; protein; 98 AA.  
 AC AAB40106;  
 XX  
 XX 05-FEB-2001 (first entry)  
 XX  
 XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 532.  
 DE  
 DE Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipapillary; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.

XX  
 OS Homo sapiens.  
 XX  
 XX WO2000056772-A1.  
 XX  
 XX 28-SEP-2000.  
 XX  
 XX 24-MAR-2000; 2000WO-US007945.  
 XX  
 XX 25-MAR-1999; 99US-0126603P.  
 XX  
 XX (BADI ) BASF AG.  
 XX (GEMY ) GENETICS INST INC.  
 XX  
 XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX  
 XX WPI; 2000-638250/61.  
 XX  
 XX New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 XX  
 XX Claim 75; Page 121; 377pp; English.  
 XX  
 XX This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
 CC C61071. The antibody of the invention is a neutralising antibody and has  
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;  
 CC neuroprotective; antipapillary; antiasthmatic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease,  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 XX disorders  
 XX  
 XX Sequence 98 AA;  
 SQ  
 Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRADTVAVY 95  
 DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRADTVAVY 95  
 QY 96 CAR 98  
 DB 96 CAR 98  
 RESULT 10  
 AAB40102  
 ID AAB40102 standard; protein; 98 AA.  
 XX  
 XX AAB40102;  
 AC  
 XX 05-FEB-2001 (first entry)  
 XX  
 XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 628.  
 DE  
 DE Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipapillary; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.

KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

XX WO200056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US007946.

XX 25-MAR-1999; 99US-0126603P.

XX (BADI ) BASF AG.

XX (GEMY ) GENETICS INST INC.

XX Salfeld JG, Roguska M, Paekind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to

XX treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 XX disease and multiple sclerosis.

XX Claim 75; Page 121; 377pp; English.

XX This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
 CC C61071. The antibody of the invention is a neutralising antibody and has  
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;  
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease,  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 CC disorders

XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVY 95

Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVY 95

QY 96 CAR 98

Db 96 CAR 98

RESULT 11

ID AAB40101 standard; protein; 98 AA.

XX AAB40101;

XX 05-FEB-2001 (first entry)  
 DT Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 627.  
 XX  
 DE Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 XX complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

XX WO200056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US007946.

XX 25-MAR-1999; 99US-0126603P.

XX (BADI ) BASF AG.

XX (GEMY ) GENETICS INST INC.

XX Salfeld JG, Roguska M, Paekind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A; AR;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to  
 XX treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 XX disease and multiple sclerosis.

XX Claim 75; Page 121; 377pp; English.

XX This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
 CC C61071. The antibody of the invention is a neutralising antibody and has  
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;  
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease,  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 CC disorders

XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVY 95

Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVY 95

QY 96 CAR 98

Db 96 CAR 98

RESULT 12  
 AAB40110  
 ID AAB40110 standard; protein; 98 AA.  
 XX  
 AC AAB40110;  
 XX  
 DT 05-FEB-2001 (first entry)  
 XX  
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 636.  
 XX  
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200056772-A1.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US007946.  
 XX  
 PR 25-MAR-1999; 99US-0126603P.  
 XX  
 PA (BADI ) BASF AG.  
 PA (GENY ) GENETICS INST INC.  
 XX  
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX  
 DR WPI; 2000-638250/61.  
 XX  
 PT New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 XX  
 PS Claim 75; Page 121; 377pp; English.  
 XX  
 CC This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
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 CC antirheumatic; antiarthritic; antisclerotic; antinflammatory;  
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease;  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 CC disorders  
 XX  
 SQ Sequence 98 AA;  
 Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 KY 36 WYRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYQMNSLRADTAVY 95  
 DB 36 WYRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYQMNSLRADTAVY 95

QY 96 CAR 98  
 DB 96 CAR 98  
 RESULT 13  
 AAB40117  
 ID AAB40117 standard; protein; 98 AA.  
 XX  
 AC AAB40117;  
 XX  
 DT 05-FEB-2001 (first entry)  
 XX  
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 643.  
 XX  
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200056772-A1.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US007946.  
 XX  
 PR 25-MAR-1999; 99US-0126603P.  
 XX  
 PA (BADI ) BASF AG.  
 PA (GENY ) GENETICS INST INC.  
 XX  
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX  
 DR WPI; 2000-638250/61.  
 XX  
 PT New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 XX  
 PS Claim 75; Page 122; 377pp; English.  
 XX  
 CC This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
 CC C61071. The antibody of the invention is a neutralising antibody and has  
 CC antirheumatic; antiarthritic; antisclerotic; antinflammatory;  
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease;  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 CC disorders  
 XX  
 SQ Sequence 98 AA;  
 Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSTKNTLYLQWNSLRADETAVYY 95  
 |||||  
 Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSTKNTLYLQWNSLRADETAVYY 95  
 |||||  
 QY 96 CAR 98  
 |||||  
 Db 96 CAR 98  
 |||||

RESULT 14  
 AAB40128  
 ID AAB40128 standard; protein; 98 AA.  
 AC AAB40128;  
 XX  
 XX 05-FEB-2001 (first entry)  
 XX  
 XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 654.  
 XX  
 XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2000056772-A1.  
 XX  
 XX 28-SEP-2000.  
 PD  
 XX  
 XX 24-MAR-2000; 2000WO-US007946.  
 XX  
 XX 25-MAR-1999; 99US-0126603P.  
 XX  
 XX (BADI ) BASF AG.  
 XX (GEMY ) GENETICS INST INC.  
 XX  
 XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX  
 DR WPI; 2000-638250/61.  
 XX  
 XX New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 PT  
 XX Claim 75; Page 122; 377pp; English.  
 XX  
 XX This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
 CC C61071. The antibody of the invention is a neutralising antibody and has  
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;  
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease,  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 CC disorders

SQ Sequence 98 AA;  
 Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53; Indels 0; Gaps 0;  
 Matches 63; Conservative 0; Mismatches 0;  
 QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSTKNTLYLQWNSLRADETAVYY 95  
 |||||  
 Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSTKNTLYLQWNSLRADETAVYY 95  
 |||||  
 QY 96 CAR 98  
 |||||  
 Db 96 CAR 98  
 |||||

RESULT 15  
 AAB40099  
 ID AAB40099 standard; protein; 98 AA.  
 XX  
 XX AAB40099;  
 XX  
 XX 05-FEB-2001 (first entry)  
 DT  
 XX  
 XX Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 625.  
 XX  
 XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2000056772-A1.  
 XX  
 XX 28-SEP-2000.  
 PD  
 XX  
 XX 24-MAR-2000; 2000WO-US007946.  
 XX  
 XX 25-MAR-1999; 99US-0126603P.  
 XX  
 XX (BADI ) BASF AG.  
 XX (GEMY ) GENETICS INST INC.  
 XX  
 XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX  
 DR WPI; 2000-638250/61.  
 XX  
 XX New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 PT  
 XX Claim 75; Page 121; 377pp; English.  
 XX  
 XX This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
 CC C61071. The antibody of the invention is a neutralising antibody and has  
 CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;  
 CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated

CC with detrimental release of human IL-12, especially Crohn's disease,  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 CC disorders  
 CC  
 CC Sequence 98 AA;  
 SQ  
 Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WVRQAPGKLEWVAIVSYDGSNKYIADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95  
 Db 36 WVRQAPGKLEWVAIVSYDGSNKYIADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95  
 QY 96 CAR 98  
 Db 96 CAR 98  
 RESULT 16  
 AAB40103  
 ID AAB40103 standard; protein; 98 AA.  
 XX  
 AC AAB40103;  
 CC  
 DT 05-FEB-2001 (first entry)  
 XX  
 DE Anti-HIL12 antibody H chain V region amino acid sequence SEQ ID 629.  
 XX  
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antiparastic; antidiabetic; cardiant;  
 KW antiparastic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200056772-A1.  
 PN  
 XX 28-SEP-2000.  
 PD  
 XX 24-MAR-2000; 2000WO-US007946.  
 PF  
 XX 25-MAR-1999; 99US-0126603P.  
 PR  
 XX (SADI ) BASF AG.  
 PA (GEMY ) GENETICS INST INC.  
 PA  
 XX Salfeld JG, Rogueka M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GW, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;  
 XX  
 DR WPI; 2000-638250/61.  
 XX  
 XX New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 PT  
 XX Claim 75; Page 121; 377pp; English.  
 PS  
 XX This invention relates to a new human antibody specific for human  
 XX interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAB61062-

CC C61071. The antibody of the invention is a neutralising antibody and has  
 CC antirheumatic; antidiabetic; antisclerotic; antidiabetic; antiparastic;  
 CC neuroprotective; antiparastic; antidiabetic; cardiant; antiparastic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease,  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 CC disorders  
 CC  
 CC Sequence 98 AA;  
 SQ

Query Match 54.8%; Score 63; DB 3; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WVRQAPGKLEWVAIVSYDGSNKYIADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95  
 Db 36 WVRQAPGKLEWVAIVSYDGSNKYIADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95  
 QY 96 CAR 98  
 Db 96 CAR 98

RESULT 17  
 AAB67512  
 ID AAB67512 standard; peptide; 98 AA.  
 XX  
 AC AAB67512;  
 CC  
 DT 29-MAY-2001 (first entry)  
 XX  
 DE Heavy chain variable region of anti-CTLA-4 antibody 3-30.3.  
 XX  
 KW Complementarity determining region; CDR; immune response; antibody;  
 KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;  
 KW autoimmune disease; infectious disease; inflammation; allergy;  
 KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;  
 KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;  
 KW transplant rejection; graft versus host disease.  
 XX  
 OS Homo sapiens.

Key Location/Qualifiers  
 Region 31..35  
 /note= "CDR1"  
 Region 50..66  
 /note= "CDR2"  
 WO200114424-A2.  
 01-MAR-2001.  
 24-AUG-2000; 2000WO-US023356.  
 24-AUG-1999; 99US-0150452P.  
 (MEDA-) MEDAREX INC.  
 Korman AJ, Halk EL, Lomberg N;  
 WPI; 2001-202933/20.

Novel human sequence antibody that binds to human cytotoxic T lymphocyte  
 associated antigen-4, useful for inducing, augmenting or prolonging  
 immune response to antigen or for suppressing immune response in patient.  
 Example 3; Fig 8; 127pp; English.  
 The present sequence represents the heavy chain variable region of human  
 antibody 3-30.3. This antibody specifically binds to human cytotoxic T  
 lymphocyte associated antigen-4 (CTLA-4). Such antibodies are used in

CC methods for inducing, augmenting or prolonging an immune response to an  
 CC antigen in a patient, where the antibodies block binding of human CTLA-4  
 CC to human B7 ligands. The antibodies are also useful for treating  
 CC autoimmune disease in a subject caused or exacerbated by increased  
 CC activity of T cells and for treating prostate cancer, melanoma or  
 CC epithelial cancer. A polyvalent or polyclonal antibody preparation  
 CC comprising two antibodies of the invention are useful for suppressing a  
 CC immune response in a patient. They are used for treating cancer,  
 CC infectious diseases and promoting beneficial autoimmune reactions for the  
 CC treatment of diseases with inflammatory or allergic components. The  
 CC polyvalent or polyclonal preparations are useful for treating autoimmune  
 CC diseases such as rheumatoid arthritis, myasthenia gravis and lupus  
 CC erythematosus, multiple sclerosis, insulin-dependent diabetes mellitus,  
 CC transplant rejection, and inflammation, graft versus host disease  
 XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 4; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95  
 Db |||||  
 QY 36 WVRQAPGKLEWVAIVSYDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95  
 Db |||||

RESULT 18  
 AAB67507  
 ID AAB67507 standard; peptide; 98 AA.  
 AC AAB67507;  
 DT 29-MAY-2001 (first entry)  
 DE Light chain variable region of anti-CTLA-4 antibody 3-30-3.  
 XX Complementarity determining region; CDR; immune response; antibody;  
 KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;  
 KW autoimmune disease; infectious disease; inflammation; allergy;  
 KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;  
 KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;  
 KW transplant rejection; graft versus host disease.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Region 31..35  
 FT /note= "CDR1"  
 FT Region 50..66  
 FT /note= "CDR2"  
 XX  
 FN WO200114424-A2.  
 XX  
 PD 01-MAR-2001.  
 XX  
 PF 24-AUG-2000; 2000WO-US023356.  
 XX  
 PR 24-AUG-1999; 99US-0150452P.  
 XX  
 PA (MEDA-) MEDAREX INC.  
 XX  
 PI Korman AJ, Halk EL, Lonberg N;  
 XX WPI; 2001-202933/20.  
 DR Novel human sequence antibody that binds to human cytotoxic T lymphocyte  
 XX associated antigen-4, useful for inducing, augmenting or prolonging  
 PT immune response to antigen or for suppressing immune response in patient.  
 XX

## Example 3; Fig 7; 127pp; English.

PS The present sequence represents the light chain variable region of human  
 XX antibody 10P1. This antibody specifically binds to human cytotoxic T  
 CC lymphocyte associated antigen-4 (CTLA-4). Such antibodies are used in  
 CC methods for inducing, augmenting or prolonging an immune response to an  
 CC antigen in a patient, where the antibodies block binding of human CTLA-4  
 CC to human B7 ligands. The antibodies are also useful for treating  
 CC autoimmune disease in a subject caused or exacerbated by increased  
 CC activity of T cells and for treating prostate cancer, melanoma or  
 CC epithelial cancer. A polyvalent or polyclonal antibody preparation  
 CC comprising two antibodies of the invention are useful for suppressing a  
 CC immune response in a patient. They are used for treating cancer,  
 CC infectious diseases and promoting beneficial autoimmune reactions for the  
 CC treatment of diseases with inflammatory or allergic components. The  
 CC polyvalent or polyclonal preparations are useful for treating autoimmune  
 CC diseases such as rheumatoid arthritis, myasthenia gravis and lupus  
 CC erythematosus, multiple sclerosis, insulin-dependent diabetes mellitus,  
 CC transplant rejection, and inflammation, graft versus host disease  
 XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 4; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95  
 Db |||||  
 QY 36 WVRQAPGKLEWVAIVSYDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVY 95  
 Db |||||

RESULT 19  
 ABG78201  
 ID ABG78201 standard; protein; 98 AA.  
 XX  
 AC ABG78201;  
 DT 15-NOV-2002 (first entry)  
 DE Human Fv molecule hypervariable region related peptide #76.  
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KW lymphoma; myeloma; blastoma; seminoma; acute myeloid leukaemia.  
 XX Homo sapiens.  
 OS  
 XX WO200259264-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 31-DEC-2001; 2001WO-US049440.  
 XX  
 PR 29-DEC-2000; 2000US-00751181.  
 XX  
 PA (BIOT-) BTO-TECHNOLOGY GEN CORP.  
 XX  
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
 PI Plaksin D, Peretz T;  
 XX WPI; 2002-619166/66.  
 DR Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 XX cells.  
 XX Claim 13; Page 186; 232pp; English.  
 XX

CC The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention  
 XX Sequence 98 AA;  
 SQ

Query Match 54.8%; Score 63; DB 5; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYY 95  
 DB 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYY 95

QY 96 CAR 98  
 DB 96 CAR 98

RESULT 20  
 ABG78199  
 ID ABG78199 standard; protein; 98 AA.  
 AC ABG78199;  
 DT 15-NOV-2002 (first entry)  
 DE Human Fv molecule hypervariable region related peptide #74.  
 KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
 OS Homo sapiens.  
 PN WO200259264-A2.  
 PD 01-AUG-2002.  
 PF 31-DEC-2001; 2001WO-US049440.  
 PR 29-DEC-2000; 2000US-00751181.  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
 PI Plaksin D, Peretz T;  
 DR WPI; 2002-619166/66.  
 PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.  
 PS Claim 13; Page 185; 232pp; English.  
 CC The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is

CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention  
 XX Sequence 98 AA;  
 SQ

Query Match 54.8%; Score 63; DB 5; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYY 95  
 DB 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYY 95

QY 96 CAR 98  
 DB 96 CAR 98

RESULT 21  
 ABG78200  
 ID ABG78200 standard; protein; 98 AA.  
 AC ABG78200;  
 DT 15-NOV-2002 (first entry)  
 DE Human Fv molecule hypervariable region related peptide #75.  
 KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
 OS Homo sapiens.  
 PN WO200259264-A2.  
 PD 01-AUG-2002.  
 PF 31-DEC-2001; 2001WO-US049440.  
 PR 29-DEC-2000; 2000US-00751181.  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
 PI Plaksin D, Peretz T;  
 DR WPI; 2002-619166/66.  
 PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.  
 PS Claim 13; Page 186; 232pp; English.  
 CC The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where

CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention  
 XX  
 SQ Sequence 98 AA;  
 Query Match 54.8%; Score 63; DB 5; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WYRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95  
 Db 36 WYRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95  
 QY 96 CAR 98  
 Db 96 CAR 98  
 RESULT 22  
 ABG91890  
 ID ABG91890 standard; protein; 98 AA.  
 AC ABG91890;  
 DT 04-DEC-2002 (first entry)  
 DE Human antibody fragment #74.  
 XX  
 KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KW myocardial infarction; retinopathic disease; abnormal platelet function;  
 KW sulphated tyrosine-dependent protein-protein interaction.  
 OS Homo sapiens.  
 XX  
 FN WO200253700-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 31-DEC-2001; 2001WO-US049442.  
 XX  
 PR 29-DEC-2000; 2000US-00751181.  
 PR 29-DEC-2000; 2000US-0258948P.  
 XX  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 XX  
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
 XX  
 DR WPI; 2002-674776/72.  
 XX  
 PT Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.  
 PS  
 PS Disclosure; Page 262; Opp; English.  
 CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-

CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents a human antibody fragment  
 CC of the invention  
 XX  
 SQ Sequence 98 AA;  
 Query Match 54.8%; Score 63; DB 5; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WYRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95  
 Db 36 WYRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY 95  
 QY 96 CAR 98  
 Db 96 CAR 98  
 RESULT 23  
 ABG91891  
 ID ABG91891 standard; protein; 98 AA.  
 AC ABG91891;  
 DT 04-DEC-2002 (first entry)  
 DE Human antibody fragment #75.  
 XX  
 KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KW myocardial infarction; retinopathic disease; abnormal platelet function;  
 KW sulphated tyrosine-dependent protein-protein interaction.  
 OS Homo sapiens.  
 XX  
 FN WO200253700-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 31-DEC-2001; 2001WO-US049442.  
 XX  
 PR 29-DEC-2000; 2000US-00751181.  
 PR 29-DEC-2000; 2000US-0258948P.  
 XX  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 XX  
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
 XX  
 DR WPI; 2002-674776/72.  
 XX  
 PT Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.  
 PS  
 PS Disclosure; Page 262-263; Opp; English.  
 CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one

antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, growth and/or replication of tumor or leukaemia cells, increase in number of tumor or leukaemia cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet adhesion or aggregation, for increasing mortality of tumor or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-leukaemia agents, or for decreasing the number of tumor or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and treating diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-protein interactions. This sequence represents a human antibody fragment of the invention

XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 5; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQWNSLRADTAVYY 95  
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQWNSLRADTAVYY 95  
QY 96 CAR 98  
DB 96 CAR 98

RESULT 24

ABG91892  
ID ABG91892 standard; protein; 98 AA.

AC ABG91892;

DT 04-DEC-2002 (first entry)

XX Human antibody fragment #76.

DE Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
KW myocardial infarction; retinopathic disease; abnormal platelet function;  
KW sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.

XX WO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

XX 29-DEC-2000; 2000US-00751181.

XX 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;  
PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
XX WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in  
PT physiological phenomena such as cell rolling, metastasis and  
PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
PT diseases, and cancer.

XX Disclosure; Page 263; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and  
CC important in physiological phenomena such as cell rolling, metastasis and  
CC inflammation, where the epitope is capable of being bound by an antibody,  
CC its antigen-binding fragment or its complex comprising at least one  
CC antibody or its binding fragment having a first hypervariable region. The  
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
CC tumor or leukaemia cells, increase in number of tumor or leukaemia  
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
CC mortality of tumor or leukaemia cells, for increasing the susceptibility  
CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
CC leukaemia agents, or for decreasing the number of tumor or leukaemia  
CC cells in a patient, or in the manufacture of a medicament for the above  
CC mentioned purposes. The epitopes are useful for diagnosing and treating  
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
CC diseases, cardiovascular diseases such as myocardial infarction,  
CC retinopathic diseases and other diseases mediated by abnormal platelet  
CC function and diseases caused by sulphated tyrosine-dependent protein-  
CC protein interactions. This sequence represents a human antibody fragment  
CC of the invention

XX Sequence 98 AA;

Query Match 54.8%; Score 63; DB 5; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQWNSLRADTAVYY 95  
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQWNSLRADTAVYY 95  
QY 96 CAR 98  
DB 96 CAR 98

RESULT 25

ABO27091  
ID ABO27091 standard; protein; 98 AA.

AC ABO27091;

XX 10-SEP-2003 (first entry)

XX Human germline heavy chain variable region gene segment #24.

XX Human; heavy chain variable region; VH; humanised antibody;  
KW chimeric antibody; complementarity determining region; CDR;  
KW canonical CDR structure type.

XX Homo sapiens.

XX US2003039649-A1.

XX 27-FEB-2003.

XX 12-JUL-2002; 2002US-00194975.

XX 12-JUL-2001; 2001US-0305111P.

XX (FOOT/) FOOTE J.

XX Foote J;

XX WPI; 2003-492151/46.

XX Making humanized antibody for converting antibody, by making chimeric  
PT antibodies containing complementarity determining region from non-human  
PT antibody and appropriate framework sequences of human antibodies.

XX Example 1; Fig 1; 31pp; English.

XX The invention describes a method of making a humanised antibody,  
 CC comprising making chimeric antibodies containing a complementarity  
 CC determining region (CDR) from a non-human antibody and appropriate  
 CC framework sequences (I) of human antibodies. (I) is selected by using  
 CC canonical CDR structure types of non-human antibody in comparison to  
 CC germline canonical CDR structure types of human antibodies as the basis  
 CC for selection, for humanisation. The method is useful for making a  
 CC humanised antibody or a converted antibody. The method is applicable for  
 CC converting a subject antibody sequence of any subject species to a less  
 CC immunogenic form suitable for use in an object species. The method is  
 CC reliable for identifying suitable human framework sequences to support  
 CC non-human CDR regions and to provide humanised antibodies that retain  
 CC high antigen binding with low immunogenicity in humans, without the need  
 CC for direct comparison of framework sequences, without the need for  
 CC determining critically important amino acid residues in the framework,  
 CC and without the need for multiple iteration and construction to obtain  
 CC humanised antibodies with suitable therapeutic properties. The antibody  
 CC has high affinity and low immunogenicity without need for comparing  
 CC framework sequences between non-human and human antibodies. This sequence  
 CC represents a human heavy chain variable region gene segment used in the  
 CC creation of humanised antibodies  
 XX SQ Sequence 98 AA;

Query Match 54.8%; Score 63; DB 6; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-53;  
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 36 WVRQAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQNSLRADTAVYY 95  
 Db 36 WVRQAPGKGLWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQNSLRADTAVYY 95  
 Qy 96 CAR 98  
 Db 96 CAR 98

Search completed: March 15, 2004, 07:38:13  
 Job time : 57 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:36:38 ; Search time 22 seconds  
(without alignments)  
269.863 Million cell updates/sec

Title: US-09-620-955b-2

Perfect score: 115

Sequence: 1 QVQLQESGGGLVPGGSLRL.....CARDRYFDLNGRGLTVSS 115

Scoring table: OLIGO

Gap 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 274646

Minimum DB seq length: 0

Maximum DB seq length: 115

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/aa/5A-COMB.pep:\*

2: /cgn2\_6/ptodata/2/aa/5B-COMB.pep:\*

3: /cgn2\_6/ptodata/2/aa/6A-COMB.pep:\*

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5: /cgn2\_6/ptodata/2/aa/PTUS-COMB.pep:\*

6: /cgn2\_6/ptodata/2/aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	54.8	98	1 US-08-211-202-118	Sequence 118, App
2	46	40.0	89	4 US-09-472-087-72	Sequence 72, Appl
3	40	34.8	95	3 US-09-043-514-2	Sequence 2, Appli
4	40	34.8	113	3 US-08-374-899-6	Sequence 6, Appli
5	32	27.8	32	1 US-08-471-780C-82	Sequence 82, Appl
6	32	27.8	32	1 US-08-467-282B-82	Sequence 82, Appl
7	32	27.8	32	2 US-08-471-282A-82	Sequence 82, Appl
8	32	27.8	32	2 US-08-466-710C-82	Sequence 82, Appl
9	32	27.8	32	2 US-08-470-139-21	Sequence 21, Appl
10	32	27.8	32	3 US-08-468-739C-82	Sequence 82, Appl
11	32	27.8	32	4 US-09-347-061-21	Sequence 21, Appl
12	31	27.0	32	1 US-07-988-925-9	Sequence 9, Appli
13	31	27.0	32	2 US-08-362-780-9	Sequence 9, Appli
14	31	27.0	87	1 US-08-497-312-21	Sequence 21, Appl
15	29	25.2	98	1 US-08-411-202-116	Sequence 116, App
16	29	25.2	112	1 US-08-411-202-133	Sequence 133, App
17	28	24.3	111	1 US-08-211-202-134	Sequence 134, App
18	27	23.5	98	1 US-07-942-245-37	Sequence 37, Appl
19	27	23.5	98	2 US-08-428-197-48	Sequence 48, Appl
20	27	23.5	98	2 US-08-665-203-31	Sequence 31, Appl
21	27	23.5	98	4 US-09-315-574-31	Sequence 31, Appl
22	27	23.5	98	5 PCT-US93-10555-48	Sequence 48, Appl
23	26	22.6	110	1 US-08-211-202-117	Sequence 117, App
24	26	22.6	111	4 US-09-266-805-6	Sequence 6, Appli
25	25	21.7	30	1 US-07-988-925-7	Sequence 7, Appli
26	25	21.7	30	2 US-08-362-780-7	Sequence 7, Appli
27	25	21.7	30	2 US-08-765-783A-92	Sequence 92, Appl

28	25	21.7	30	2	US-08-470-139-17	Sequence 17, Appl
29	25	21.7	30	3	US-09-416-557-92	Sequence 92, Appl
30	25	21.7	30	4	US-08-347-051-17	Sequence 17, Appl
31	25	21.7	87	3	US-08-765-783A-105	Sequence 105, App
32	25	21.7	87	3	US-09-416-557-105	Sequence 105, App
33	25	21.7	108	4	US-09-899-896-9	Sequence 9, Appli
34	25	21.7	109	2	US-08-428-197-3	Sequence 3, Appli
35	25	21.7	109	5	PCT-US93-10555-3	Sequence 3, Appli
36	25	21.7	111	4	US-09-899-896-7	Sequence 7, Appli
37	25	21.7	115	2	US-08-428-197-42	Sequence 42, Appl
38	25	21.7	115	5	PCT-US93-10555-42	Sequence 42, Appl
39	24	20.9	129	1	US-08-471-780C-119	Sequence 119, App
40	24	20.9	29	2	US-08-467-282B-119	Sequence 119, App
41	24	20.9	29	2	US-08-471-282A-119	Sequence 119, App
42	24	20.9	29	2	US-08-466-710C-119	Sequence 119, App
43	24	20.9	29	3	US-08-468-739C-119	Sequence 119, App
44	24	20.9	51	2	US-08-785-179B-3	Sequence 3, Appli
45	24	20.9	62	1	US-08-162-102C-41	Sequence 41, Appl
46	24	20.9	108	2	US-08-428-197-4	Sequence 4, Appli
47	24	20.9	108	5	PCT-US93-10555-4	Sequence 4, Appli
48	23	20.0	113	4	US-09-530-139-59	Sequence 59, Appli
49	23	20.0	113	4	US-09-530-139-59	Sequence 59, Appli
50	22	19.1	114	3	US-08-545-809A-124	Sequence 124, App
51	21	18.3	26	1	US-08-471-780C-80	Sequence 80, Appl
52	21	18.3	26	1	US-08-467-282B-80	Sequence 80, Appl
53	21	18.3	26	1	US-08-471-282A-80	Sequence 80, Appl
54	21	18.3	26	2	US-08-466-710C-80	Sequence 80, Appl
55	21	18.3	26	3	US-08-468-739C-80	Sequence 80, Appl
56	21	18.3	109	2	US-08-379-057-32	Sequence 32, Appl
57	20	17.4	32	4	US-09-425-638A-108	Sequence 108, App
58	20	17.4	32	4	US-09-425-638A-109	Sequence 109, App
59	20	17.4	32	4	US-09-425-638A-111	Sequence 111, App
60	20	17.4	32	4	US-09-425-638A-113	Sequence 113, App
61	20	17.4	32	4	US-09-425-638A-117	Sequence 117, App
62	20	17.4	32	4	US-09-425-638A-121	Sequence 121, App
63	20	17.4	32	4	US-09-543-004-108	Sequence 108, App
64	20	17.4	32	4	US-09-543-004-109	Sequence 109, App
65	20	17.4	32	4	US-09-543-004-111	Sequence 111, App
66	20	17.4	32	4	US-09-543-004-113	Sequence 113, App
67	20	17.4	32	4	US-09-543-004-117	Sequence 117, App
68	20	17.4	32	4	US-09-543-004-121	Sequence 121, App
69	20	17.4	115	2	US-08-379-057-31	Sequence 31, Appl
70	20	17.4	115	2	US-08-545-809A-122	Sequence 122, App
71	19	16.5	32	4	US-09-425-638A-112	Sequence 112, App
72	19	16.5	32	4	US-09-425-638A-115	Sequence 115, App
73	19	16.5	32	4	US-09-425-638A-119	Sequence 119, App
74	19	16.5	32	4	US-09-425-638A-123	Sequence 123, App
75	19	16.5	32	4	US-09-543-004-112	Sequence 112, App
76	19	16.5	32	4	US-09-543-004-115	Sequence 115, App
77	19	16.5	32	4	US-09-543-004-119	Sequence 119, App
78	19	16.5	32	4	US-09-543-004-123	Sequence 123, App
79	19	16.5	35	2	US-08-765-179B-1	Sequence 1, Appli
80	19	16.5	114	2	US-08-887-352B-11	Sequence 11, Appl
81	19	16.5	114	2	US-08-887-352B-12	Sequence 12, Appl
82	19	16.5	114	3	US-09-109-207C-11	Sequence 11, Appl
83	19	16.5	114	3	US-09-109-207C-12	Sequence 12, Appl
84	19	16.5	114	3	US-09-296-005-11	Sequence 11, Appl
85	19	16.5	114	3	US-09-296-005-12	Sequence 12, Appl
86	19	16.5	114	4	US-09-920-171-11	Sequence 11, Appl
87	19	16.5	114	4	US-09-920-171-12	Sequence 12, Appl
88	19	16.5	114	1	US-07-942-245-19	Sequence 19, Appl
89	17	14.8	17	4	US-09-383-667-16	Sequence 16, Appl
90	17	14.8	30	4	US-09-425-638A-99	Sequence 99, Appl
91	17	14.8	30	4	US-09-543-004-99	Sequence 99, Appl
92	17	14.8	67	1	US-08-162-102C-36	Sequence 36, Appl
93	17	14.8	100	1	US-08-320-515B-2	Sequence 2, Appli
94	17	14.8	100	1	US-08-309-025-2	Sequence 18, Appl
95	16	13.9	32	4	US-09-383-667-18	Sequence 18, Appl
96	16	13.9	32	4	US-09-425-638A-110	Sequence 110, App
97	16	13.9	32	4	US-09-425-638A-114	Sequence 114, App
98	16	13.9	32	4	US-09-425-638A-118	Sequence 118, App
99	16	13.9	32	4	US-09-425-638A-122	Sequence 122, App
100	16	13.9	32	4	US-09-543-004-110	Sequence 110, App



## ALIGNMENTS

## RESULT 1

US-08-211-202-118  
; Sequence 118, Application US/08211202  
; Patent No. 5565332  
; GENERAL INFORMATION:  
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus  
; APPLICANT: BAIER, Michael  
; APPLICANT: JESPERS, Laurent Stephane Anne Therese  
; APPLICANT: WINTER, Gregory Paul  
; TITLE OF INVENTION: Production of chimeric antibodies - a  
; TITLE OF INVENTION: combinatorial approach  
; NUMBER OF SEQUENCES: 144  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/211,202  
; FILING DATE: 23-SEP-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9120252.3  
; FILING DATE: 23-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9120377.8  
; FILING DATE: 25-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206372.6  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David W. Clough  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/POCKET NUMBER: 28111/31960  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 118:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-211-202-118

Query Match 54.8%; Score 63; DB 1; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.2e-48;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQMSLRADTAVYY 95  
36 WVRQAPGKLEWAVISYDGSNKYADSVKGRFTISRDNSKNTLYLQMSLRADTAVYY 95

OY  
DB

OY 96 CAR 98  
DB 96 CAR 98

## RESULT 2

US-09-472-087-72  
; Sequence 72, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, ELLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 72  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-72

Query Match 40.0%; Score 46; DB 4; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.9e-33;  
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
53 YDGSNKYADSVKGRFTISRDNSKNTLYLQMSLRADTAVYYCAR 98  
44 YDGSNKYADSVKGRFTISRDNSKNTLYLQMSLRADTAVYYCAR 89

OY  
DB

## RESULT 3

US-09-043-514-2  
; Sequence 2, Application US/09043514A  
; Patent No. 6153745  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAMS, David  
; APPLICANT: BROWN, Daniel  
; APPLICANT: ZACCOLO, Manuela C.  
; APPLICANT: GHERARDI, Ezmaning  
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO MUTAGENESIS OF NUCLEIC  
; FILE REFERENCE: 41301/251704  
; CURRENT APPLICATION NUMBER: US/09/043,514A  
; CURRENT FILING DATE: 1998-07-06  
; EARLIER APPLICATION NUMBER: GB 9519425.4  
; EARLIER FILING DATE: 1995-09-22  
; EARLIER APPLICATION NUMBER: GB 9602011.0  
; EARLIER FILING DATE: 1996-02-01  
; EARLIER APPLICATION NUMBER: PCT/GB96/02333  
; EARLIER FILING DATE: 1996-09-19  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-043-514-2

Query Match 34.8%; Score 40; DB 3; Length 95;

Best Local Similarity 100.0%; Pred. No. 3.7e-28;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98  
Db |||||  
53 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 92  
|||

RESULT 4  
US-08-974-899-6  
; Sequence 6, Application US/08974899  
; Patent No. 6037454  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Gardieu, Paula M.  
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,899  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/031971  
; FILING DATE: 11/27/96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1014R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-974-899-6

Query Match 34.8%; Score 40; DB 3; Length 113;  
Best Local Similarity 100.0%; Pred. No. 4.3e-28;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98  
Db |||||  
53 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98  
|||

RESULT 5  
US-08-471-780C-82  
; Sequence 82, Application US/08471780C  
; Patent No. 5759808  
; GENERAL INFORMATION:  
; APPLICANT: Casterman, Cecile  
; APPLICANT: Hamers, Raymond  
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.

COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,780C  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/106,944  
FILING DATE: 17-AUG-1993  
APPLICATION NUMBER: FR 92402326.0  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93401310.3  
FILING DATE: 21-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E.R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 04958.0008-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-780C-82

Query Match 27.8%; Score 32; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 RETISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98  
Db |||||  
1 RETISRDNSKNTLYLQMNSLRAEDTAVYYCAR 32  
|||

RESULT 6  
US-08-467-282B-82  
; Sequence 82, Application US/08467282B  
; Patent No. 5800988  
; GENERAL INFORMATION:  
; APPLICANT: Casterman, Cecile  
; APPLICANT: Hamers, Raymond  
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,282B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/106,944  
FILING DATE: 17-AUG-1993  
APPLICATION NUMBER: FR 92402326.0

```
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-467-282B-82

Query Match      27.8%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 98
Db      1 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 32

RESULT 7
US-08-471-282A-82
; Sequence 82, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-710C-82

Query Match      27.8%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 98
Db      1 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 32

RESULT 9
US-08-466-710C-82
; Sequence 82, Application US/08466710C
; Patent No. 5874541
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,710C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-710C-82

Query Match      27.8%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 98
Db      1 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 32

RESULT 9
```

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-282A-82

Query Match      27.8%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 98
Db      1 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 32

RESULT 8
US-08-466-710C-82
; Sequence 82, Application US/08466710C
; Patent No. 5874541
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,710C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-710C-82

Query Match      27.8%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 98
Db      1 RFTISRDNSKNTLYLQMSLRAEDTAVVYCAR 32

RESULT 9
```

US-08-470-139-21  
; Sequence 21, Application US/08470139  
; Patent No. 599586  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-470-139-21  
Query Match 27.8%; Score 32; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 67 RTISRDNSKNTLYLQMSLRADTAVYYCAR 98  
DB 1 RTISRDNSKNTLYLQMSLRADTAVYYCAR 32  
RESULT 10  
US-08-468-739C-82  
; Sequence 82, Application US/08468739C  
; Patent No. 6015695  
; GENERAL INFORMATION:  
; APPLICANT: Gasterman, Cecile  
; APPLICANT: Hamers, Raymond  
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
; NUMBER OF SEQUENCES: 130  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,739C  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/106,944  
; FILING DATE: 17-AUG-1993  
; APPLICATION NUMBER: FR 92402326.0  
; FILING DATE: 21-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93401310.3  
; FILING DATE: 21-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E.R.

US-08-468-739C-82  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 04958.0008-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-468-739C-82  
Query Match 27.8%; Score 32; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 67 RTISRDNSKNTLYLQMSLRADTAVYYCAR 98  
DB 1 RTISRDNSKNTLYLQMSLRADTAVYYCAR 32  
RESULT 11  
US-09-347-061-21  
; Sequence 21, Application US/09347061  
; Patent No. 6316227  
; GENERAL INFORMATION:  
; APPLICANT: Bodmer, Mark  
; APPLICANT: Athwal, Diljeet Singh  
; APPLICANT: Emtage, John Spencer  
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies  
; FILE REFERENCE: CARP-0071  
; CURRENT APPLICATION NUMBER: US/09/347,061  
; CURRENT FILING DATE: 1999-07-02  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 21  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Consensus  
US-09-347-061-21  
Query Match 27.8%; Score 32; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 67 RTISRDNSKNTLYLQMSLRADTAVYYCAR 98  
DB 1 RTISRDNSKNTLYLQMSLRADTAVYYCAR 32  
RESULT 12  
US-07-988-925-9  
; Sequence 9, Application US/07988925  
; Patent No. 5585097  
; GENERAL INFORMATION:  
; APPLICANT: Bolt, Sarah L  
; APPLICANT: Clark, Michael R  
; APPLICANT: Gorman, Scott D  
; APPLICANT: Routledge, Edward G  
; APPLICANT: Waldmann, Herman  
; TITLE OF INVENTION: antibody preparation  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon and Vanderhye pc  
; STREET: 11th Floor, 1100 No. 5585097th Glebe Road  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA

ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/988,925  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206422.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB92/01933  
FILING DATE: 21-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Mitchard, Leonard C  
REGISTRATION NUMBER: 29009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-988-925-9

Query Match 27.0%; Score 31; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.3e-20;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 67 RFTISRDNSKNTLYLQMSLRADTAVYYCA 97  
|||||  
Db 1 RFTISRDNSKNTLYLQMSLRADTAVYYCA 31

RESULT 13  
US-08-362-780-9  
Sequence 9, Application US/08362780  
Patent No. 5968509  
GENERAL INFORMATION:  
APPLICANT: Gorman, Scott D  
APPLICANT: Routledge, Edward G  
APPLICANT: Waldmann, Herman  
TITLE OF INVENTION: Antibody Preparation  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon and Vanderhye pc  
STREET: 8th Floor, 1100 No. 5968509th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,780  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/862,543  
FILING DATE: 23-JUNE-1992  
APPLICATION NUMBER: GB 9021679.7  
FILING DATE: 05-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB91/01726

FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Mitchard, Leonard C  
REGISTRATION NUMBER: 29009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 7038164000  
TELEFAX: 7038164100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-362-780-9

Query Match 27.0%; Score 31; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.3e-20;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 67 RFTISRDNSKNTLYLQMSLRADTAVYYCA 97  
|||||  
Db 1 RFTISRDNSKNTLYLQMSLRADTAVYYCA 31

RESULT 14  
US-08-497-312-21  
Sequence 21, Application US/08497312  
Patent No. 5712120  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Method for obtaining modified  
TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine  
TITLE OF INVENTION: antibody variable domains, compositions containing them.  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR  
STREET: 215 Y 15, ATABEY PLAYA  
CITY: HAVANA  
STATE:  
COUNTRY: CUBA  
ZIP: 11600  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/497,312  
FILING DATE: 30-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: CU 80/94  
FILING DATE: 30-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BOND, LAURENCE B.  
REGISTRATION NUMBER: 30,549  
REFERENCE/DOCKET NUMBER: 2629US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 801/532-1922  
TELEFAX: 801/531-9168  
TELEX: 388961 1PMO4UT  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 87 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-497-312-21

Query Match 27.0%; Score 31; DB 1; Length 87;  
Best Local Similarity 100.0%; Pred. No. 2.9e-20;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 RTISRDNSKNTLYLQMSLRAEDTAVYYCA 97  
|||||  
DB 45 RTISRDNSKNTLYLQMSLRAEDTAVYYCA 75  
|||||

RESULT 15  
US-08-211-202-116  
; Sequence 116, Application US/08211202  
; Patent No. 5565332  
; GENERAL INFORMATION:  
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus  
; APPLICANT: BAIER, Michael  
; APPLICANT: JESPER, Laurent Stephane Anne Therese  
; APPLICANT: WINTER, Gregory Paul  
; TITLE OF INVENTION: Production of chimeric antibodies - a  
; TITLE OF INVENTION: combinatorial approach  
; NUMBER OF SEQUENCES: 144  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &  
; ADDRESSEE: Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/211,202  
; FILING DATE: 23-SEP-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: GB 9120252.3  
; FILING DATE: 23-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9120252.3  
; FILING DATE: 23-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9120377.8  
; FILING DATE: 25-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9120377.8  
; FILING DATE: 25-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206372.6  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206372.6  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David W. Clough  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/31960  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 116:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-211-202-116

Query Match 25.2%; Score 29; DB 1; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVPGGSLRLSCAASGFTFSYSY 34  
|||||  
DB 6 ESGGGLVPGGSLRLSCAASGFTFSYSY 34  
|||||

RESULT 16  
US-08-211-202-133  
; Sequence 133, Application US/08211202  
; Patent No. 5565332  
; GENERAL INFORMATION:  
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus  
; APPLICANT: BAIER, Michael  
; APPLICANT: JESPER, Laurent Stephane Anne Therese  
; APPLICANT: WINTER, Gregory Paul  
; TITLE OF INVENTION: Production of chimeric antibodies - a  
; TITLE OF INVENTION: combinatorial approach  
; NUMBER OF SEQUENCES: 144  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &  
; ADDRESSEE: Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/211,202  
; FILING DATE: 23-SEP-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: GB 9120252.3  
; FILING DATE: 23-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9120377.8  
; FILING DATE: 25-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206372.6  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David W. Clough  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/31960  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 133:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-211-202-133

Query Match 25.2%; Score 29; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 2e-18;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVPGGSLRLSCAASGFTFSYSY 34  
|||||  
DB 6 ESGGGLVPGGSLRLSCAASGFTFSYSY 34  
|||||

RESULT 17  
US-08-211-202-134  
; Sequence 134, Application US/08211202  
; Patent No. 5565332  
; GENERAL INFORMATION:  
; APPLICANT: HOOGENDOORN, Hendricus Renerus Jacobus Mattheus  
; APPLICANT: BAIER, Michael  
; APPLICANT: JESPER, Laurent Stephane Anne Therese  
; APPLICANT: WINTER, Gregory Paul  
; TITLE OF INVENTION: Production of chimeric antibodies - a  
; TITLE OF INVENTION: combinatorial approach  
; NUMBER OF SEQUENCES: 144  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &  
; ADDRESS: Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/211,202  
; FILING DATE: 23-SEP-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9120252.3  
; FILING DATE: 23-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9120377.8  
; FILING DATE: 25-SEP-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206372.6  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David W. Clough  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/31960  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 134:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-211-202-134  
Query Match 24.3%; Score 28; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 SGGLVQPGSURLSCAASGTFSSY 34  
DB 7 SGGLVQPGSURLSCAASGTFSSY 34  
  
RESULT 18  
US-07-942-245-37  
; Sequence 37, Application US/07942245  
; Patent No. 5639641

; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, Jan T.  
; APPLICANT: SEARLE, Stephen M.J.  
; APPLICANT: REES, Anthony R.  
; APPLICANT: ROGUSKA, Michael A.  
; APPLICANT: GUILD, Braydon C.  
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 522  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: HP 9000/700 Workstation  
; OPERATING SYSTEM: UNIX  
; SOFTWARE: In house  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/942,245  
; FILING DATE: 09-SEP-1992  
; CLASSIFICATION: 530  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 293-7060  
; TELEFAX: (202) 293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
US-07-942-245-37  
Query Match 23.5%; Score 27; DB 1; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1e-16;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 ESGGLVQPGSURLSCAASGTFSSY 32  
DB 6 ESGGLVQPGSURLSCAASGTFSSY 32  
  
RESULT 19  
US-08-428-197-48  
; Sequence 48, Application US/08428197  
; Patent No. 5891438  
; GENERAL INFORMATION:  
; APPLICANT: SILVERMAN, GREGG J.  
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH  
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Spensley Horn Jubas & Lubitz  
; STREET: 1880 Century Park East - Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90067  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/428,197  
; FILING DATE:  
; CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Howells, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: FD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-428-197-48

Query Match 23.5%; Score 27; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1e-16;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGSLRLSCAASGFTSSY 32  
DB 6 ESGGGLVQPGGSLRLSCAASGFTSSY 32

RESULT 20  
US-08-665-202-31  
Sequence 31, Application US/08665202  
Patent No. 597322  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 597322el High Affinity Human Antibodies to  
TITLE OF INVENTION: Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,202  
FILING DATE: 13-JUN-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061410  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-428-197-48

US-08-665-202-31  
Query Match 23.5%; Score 27; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1e-16;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGSLRLSCAASGFTSSY 32  
DB 6 ESGGGLVQPGGSLRLSCAASGFTSSY 32

RESULT 21  
US-09-315-574-31  
Sequence 31, Application US/09315574  
Patent No. 6512097  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to  
TITLE OF INVENTION: Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.  
STREET: Four Embarcadero Center, Suite 1100  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4106  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/315,574  
FILING DATE: 20-MAY-99  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/665,202  
FILING DATE: 13-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061411  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-315-574-31

Query Match 23.5%; Score 27; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1e-16;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGSLRLSCAASGFTSSY 32  
DB 6 ESGGGLVQPGGSLRLSCAASGFTSSY 32

RESULT 22  
PCT-US93-10555-48



Sequence 48, Application PC/TUS9310555  
GENERAL INFORMATION:  
APPLICANT: SILVERMAN, GREGG J.  
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH  
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Howells, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: PD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-10555-48

Query Match 23.5%; Score 27; DB 5; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1e-16;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32  
Db 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32

RESULT 23  
US-08-211-202-117  
Sequence 117, Application US/08211202  
Patent No. 5565332  
GENERAL INFORMATION:  
APPLICANT: HOGENBOOM, Hendricus Renerus Jacobus Matteus  
APPLICANT: BAER, Michael  
APPLICANT: JESPER, Laurent Stephane Anne Therese  
APPLICANT: WINTER, Gregory Paul  
TITLE OF INVENTION: Production of chimeric antibodies - a  
TITLE OF INVENTION: combinatorial approach  
NUMBER OF SEQUENCES: 144  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &  
ADDRESSEE: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/211,202  
FILING DATE: 23-SEP-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9120252.3  
FILING DATE: 23-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9120377.8  
FILING DATE: 25-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/00883  
FILING DATE: 15-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/31960  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-211-202-117

Query Match 22.6%; Score 26; DB 1; Length 110;  
Best Local Similarity 100.0%; Pred. No. 8.7e-16;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGGGLVQPGGSLRLSCAASGFTFSY 32  
Db 7 SGGGLVQPGGSLRLSCAASGFTFSY 32

RESULT 24  
US-09-266-805-6  
Sequence 6, Application US/09266805  
Patent No. 6517829  
GENERAL INFORMATION:  
APPLICANT: Unilever N.V.  
APPLICANT: Unilever PLC  
TITLE OF INVENTION: New products comprising inactivated yeasts or moulds  
TITLE OF INVENTION: provided with active antibodies  
FILE REFERENCE: t-7055  
CURRENT APPLICATION NUMBER: US/09/266,805  
CURRENT FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 111  
TYPE: PPT  
ORGANISM: llama  
US-09-266-805-6

Query Match 22.6%; Score 26; DB 4; Length 111;  
Best Local Similarity 100.0%; Pred. No. 8.7e-16;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGGGLVQPGGSLRLSCAASG 26  
Db 1 QVQLQESGGGLVQPGGSLRLSCAASG 26

RESULT 25  
US-07-988-925-7  
; Sequence 7, Application US/07988925  
; Patent No. 5585097  
; GENERAL INFORMATION:  
; APPLICANT: Bolt, Sarah L  
; APPLICANT: Clark, Michael R  
; APPLICANT: Gorman, Scott D  
; APPLICANT: Routledge, Edward G  
; APPLICANT: Waldmann, Herman  
; TITLE OF INVENTION: antibody preparation  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon and Vanderhye PC  
; STREET: 11th Floor, 1100 No. 5585097th Glebe Road  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/988,925  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206422.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/GB92/01933  
; FILING DATE: 21-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mitchard, Leonard C  
; REGISTRATION NUMBER: 29009  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 7038164000  
; TELEFAX: 7038164100  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-988-925-7

Query Match 21.7%; Score 25; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred.No. 2.3e-15;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 BSGGGLVPGGSLRLSCAASGFTFS 30  
|||  
Db 6 BSGGGLVPGGSLRLSCAASGFTFS 30  
|||

Search completed: March 15, 2004, 07:40:10  
Job time : 23 secs



## ALIGNMENTS

## RESULT 1

PH1645  
Ig heavy chain V region (clone 6C8) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C:Accession: PH1645  
R:Hallson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A  
A:Reference number: PH1642; MUID:93301610; PMID:8315388  
A:Accession: PH1645  
A:Molecule type: mRNA  
A:Residues: 1-111 <HL>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 55.5%; Score 65; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 4.7e-59;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95  
DB 28 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 87

QY 96 CARD 100  
DB 88 CARD 92

## RESULT 2

PH1646  
Ig heavy chain V region (clone 6H12) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C:Accession: PH1646  
R:Hallson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A  
A:Reference number: PH1642; MUID:93301610; PMID:8315388  
A:Accession: PH1646  
A:Molecule type: mRNA  
A:Residues: 1-109 <HL>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 55.7%; Score 64; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 4.8e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95  
DB 28 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 87

QY 96 CARD 99  
DB 88 CARD 91

## RESULT 3

S46390  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C>Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S46390  
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
A:Reference number: S46390; MUID:94254092; PMID:8196048

A:Accession: S46390  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <FIG>  
A:Cross-references: EMBL:Z31686; NID:G509782; PIDN:CAA83493.1; PID:gl335143  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 55.7%; Score 64; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 5e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95  
DB 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95

QY 96 CARD 99  
DB 96 CARD 99

## RESULT 4

S46392  
Ig heavy chain V region (VH-28) - human  
C:Species: Homo sapiens (man)  
C>Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S46392  
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
A:Reference number: S46390; MUID:94254092; PMID:8196048  
A:Accession: S46392  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <FIG>

A:Cross-references: EMBL:Z31688; NID:G499306; PIDN:CAA83493.1; PID:gl335145  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 55.7%; Score 64; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 5e-58;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95  
DB 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQNSLRAEDTAVYY 95

QY 96 CARD 99  
DB 96 CARD 99

## RESULT 5

S29546  
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 07-Jan-1994 #sequence\_revision 17-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S29546; S26888  
R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S29543  
A:Accession: S29546  
A:Molecule type: DNA  
A:Residues: 1-98 <TOM>

A:Cross-references: EMBL:Z17394; NID:G32843; PIDN:CAA78997.1; PID:G32844  
A>Note: designated COS-8  
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A:Title: The repertoire of human germline VH sequences reveals about fifty groups of  
A:Reference number: S26885; MUID:93021117; PMID:1404388  
A:Accession: S26888

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-98 <TOW>  
A;Cross-references: EMBL:Z12346; NID:G32912; PIDN:CAA78216.1; PID:G32913  
A;Note: designated DP-46  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMV>

Query Match 54.8%; Score 63; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 4.7e-57;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95  
|||  
Db 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95  
|||

Qy 96 CAR 98  
|||  
Db 96 CAR 98  
|||

RESULT 6  
PH1644  
Ig heavy chain V region (clone 5D11) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C;Accession: PH1644  
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, B.H.  
J. Exp. Med. 178, 331-336, 1993  
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A  
A;Reference number: PH1642; MUID:93301610; PMID:8315388  
A;Accession: PH1644  
A;Molecule type: mRNA  
A;Residues: 1-109 <HIL>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;7-90/Domain: immunoglobulin homology <IMV>

Query Match 54.8%; Score 63; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 5.1e-57;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95  
|||  
Db 28 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 87  
|||

Qy 96 CAR 98  
|||  
Db 88 CAR 90  
|||

RESULT 7  
PL0116  
Ig heavy chain V-III region (AW-Vx) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 23-Jul-1999  
C;Accession: PL0116; S26892  
R;Bird, J.; Gallil, N.; Link, M.; Stites, D.; Sklar, J.  
J. Exp. Med. 168, 229-245, 1988  
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin heavy chain V region  
A;Reference number: PL0116; MUID:88286083; PMID:2840480  
A;Accession: PL0116  
A;Molecule type: mRNA  
A;Residues: 1-98 <BIR>  
A;Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL  
A;Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline VH sequences reveals about fifty groups of V region segments  
A;Reference number: S26895; MUID:93021117; PMID:11404388  
A;Accession: S26892  
A;Status: preliminary

A;Molecule type: DNA  
A;Residues: 1-98 <TOW>  
A;Cross-references: EMBL:Z12349; NID:G32918; PIDN:CAA78219.1; PID:G32919  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMV>  
F;31-35/Region: complementarity-determining 1  
F;49-65/Region: complementarity-determining 2

Query Match 53.9%; Score 62; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 5e-56;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95  
|||  
Db 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95  
|||

Qy 96 CA 97  
|||  
Db 96 CA 97  
|||

RESULT 8  
PH1643  
Ig heavy chain V region (clone 6H7) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C;Accession: PH1643  
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A  
A;Reference number: PH1642; MUID:93301610; PMID:8315388  
A;Accession: PH1643  
A;Molecule type: mRNA  
A;Residues: 1-111 <HIL>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;7-90/Domain: immunoglobulin homology <IMV>

Query Match 53.9%; Score 62; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 5.5e-56;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95  
|||  
Db 28 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 87  
|||

Qy 96 CA 97  
|||  
Db 88 CA 89  
|||

RESULT 9  
S44115  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C;Accession: S44115  
R;Hawkins, R.E.; Zhu, D.; Oveska, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable region  
A;Reference number: S44105  
A;Accession: S44115  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-97 <HAW>  
A;Cross-references: EMBL:Z31384; NID:G472969; PIDN:CAA83259.1; PID:G940526  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 52.2%; Score 60; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 5.5e-54;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYY 95  
 |||||  
 Db 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYY 95  
 |||||

## RESULT 10

PL0120  
 IG heavy chain V-III region (TD-Vo) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 16-Aug-1996  
 C:Accession: P10120  
 R:Bird, J.; Galli, N.; Link, M.; Stites, D.; Sklar, J.  
 J. Exp. Med. 168, 229-245, 1988  
 A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin  
 A:Reference number: PL0116; MUID:88286083; PMID:2840480  
 A:Accession: P10120  
 A:Molecule type: mRNA  
 A:Residues: 1-94 <BIR>  
 A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL  
 A>Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin  
 F:31-35/Region: complementarity-determining 1  
 F:49-65/Region: complementarity-determining 2

Query Match 51.3%; Score 59; DB 2; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-53;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 94  
 |||||  
 Db 36 WVRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVY 94  
 |||||

## RESULT 11

PH1642  
 IG heavy chain V region (clone 5A10) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
 C:Accession: PH1642  
 R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.  
 J. Exp. Med. 178, 331-336, 1993  
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo  
 A:Reference number: PH1642; MUID:93301610; PMID:8315388  
 A:Accession: PH1642  
 A:Molecule type: mRNA  
 A:Residues: 1-108 <HIL>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 40.9%; Score 47; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-40;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCARD 99  
 |||||  
 Db 45 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCARD 91  
 |||||

## RESULT 12

S46391  
 IG heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
 C:Accession: S46391  
 R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
 J. Mol. Biol. 239, 68-78, 1994  
 A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
 A:Reference number: S46390; MUID:94254092; PMID:8196048  
 A:Accession: S46391  
 A>Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-114 <FIG>  
 A:Cross-references: EMBL:Z31687; NID:G509784; PIDN:CAA83492.1; PID:gl335144  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-96/Domain: immunoglobulin homology <IMM>

Query Match 40.9%; Score 47; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-40;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCARD 99  
 |||||  
 Db 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCARD 99  
 |||||

## RESULT 13

S29543  
 IG heavy chain V region (COS 3) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 07-Jan-1994 #sequence\_revision 17-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S29543  
 R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.  
 submitted to the EMBL Data Library, October 1992  
 A:Reference number: S29543  
 A:Accession: S29543  
 A:Molecule type: DNA  
 A:Residues: 1-98 <TOM>

A:Cross-references: EMBL:Z17989; NID:G32835; PIDN:CAA78994.1; PID:G32836  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 45; DB 2; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-38;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCA 97  
 |||||  
 Db 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCA 97  
 |||||

## RESULT 14

S26935  
 IG heavy chain V region (DP-42) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S26935

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.  
 J. Mol. Biol. 227, 776-798, 1992  
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-97 <TOM>

A:Cross-references: EMBL:Z12342; NID:G32905; PIDN:CAA78212.1; PID:G32906  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 40; DB 2; Length 97;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCAR 98  
 |||||  
 Db 58 YYADSVKGRFTISRDNKNTLYLQMSLRADTAVYYCAR 97  
 |||||

## RESULT 15

S46462  
 IG heavy chain V region (YAC-5) - human

C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C;Accession: S46462  
R;Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Win  
Nature Genet. 7, 162-168, 1994  
A;Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom  
A;Reference number: S46460; PMID:95004581; PMID:7920635  
A;Accession: S46462  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-97 <COO>  
A;Cross-references: EMBL:Z27504; NID:G505430; PIDN:CAA81824.1; PID:G505431  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
P;15-97/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 40; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 98  
Db 58 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 97

RESULT 16  
S24249  
IG heavy chain V region (VH26-DNI-DXP1-JH4) - human  
C;Species: Homo sapiens (man)  
C;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 30-May-1997  
C;Accession: S24249  
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.  
submitted to the EMBL Data Library, June 1992  
A;Description: A single VH gene predominates in the rearranged and expressed human B cell  
A;Reference number: S24247  
A;Accession: S24249  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-105 <STE>  
A;Cross-references: EMBL:X67070  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
P;10-92/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 40; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.8e-33;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 98  
Db 53 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 92

RESULT 17  
S26889  
IG heavy chain V region (DP-47) - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S26889  
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A;Reference number: S26885; PMID:93021117; PMID:1404388  
A;Accession: S26889  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-98 <TOM>  
A;Cross-references: EMBL:Z12347; NID:G32914; PIDN:CAA78217.1; PID:G32915  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
P;15-98/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 1.8e-32;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 97  
Db 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 97

RESULT 18  
S24259  
IG heavy chain V region (VH26-DX1-JH4) - human  
C;Species: Homo sapiens (man)  
C;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S24259  
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.  
submitted to the EMBL Data Library, June 1992  
A;Description: A single VH gene predominates in the rearranged and expressed human B cell  
A;Reference number: S24247  
A;Accession: S24259  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-99 <STE>  
A;Cross-references: EMBL:X67067; NID:G38391; PIDN:CAA47452.1; PID:G38392  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
P;1-83/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.8e-32;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 97  
Db 44 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 82

RESULT 19  
S24258  
IG heavy chain V region (VH26-DXP1-JH4) - human  
C;Species: Homo sapiens (man)  
C;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S24258  
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.  
submitted to the EMBL Data Library, June 1992  
A;Description: A single VH gene predominates in the rearranged and expressed human B cell  
A;Reference number: S24247  
A;Accession: S24258  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-100 <STE>  
A;Cross-references: EMBL:X67066; NID:G38389; PIDN:CAA47451.1; PID:G38390  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
P;4-86/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 100;  
Best Local Similarity 100.0%; Pred. No. 1.8e-32;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 97  
Db 47 YYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCA 85

RESULT 20  
S24257  
IG heavy chain V region (VH26-DXP1-JH4) - human  
C;Species: Homo sapiens (man)  
C;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C;Accession: S24257  
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.  
submitted to the EMBL Data Library, June 1992  
A;Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24257

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-101 <STE>

A:Cross-references: EMBL:X67065; NID:G38387; PIDN:CAA47450.1; PID:G38388

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-93/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 1.9e-32;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 97

DB 54 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 92

RESULT 21

S24260

IG heavy chain V region (VH26-DAL-JH4) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 06-Jun-1997

C:Accession: S24260

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24260

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-102 <STE>

A:Cross-references: EMBL:X67068

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:5-87/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 102;  
Best Local Similarity 100.0%; Pred. No. 1.9e-32;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 97

DB 48 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 86

RESULT 22

S24255

IG heavy chain V region (VH26-DLR5-JH4) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 06-Jun-1997

C:Accession: S24255

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24255

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-104 <STE>

A:Cross-references: EMBL:X67063

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:2-84/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.9e-32;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 97

DB 45 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 83

RESULT 23

S24256

IG heavy chain V region (VH26-DXP4-JH6) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S24256

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24256

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-106 <STE>

A:Cross-references: EMBL:X67064; NID:G38385; PIDN:CAA47449.1; PID:G38386

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:4-86/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.9e-32;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 97

DB 47 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 85

RESULT 24

PH1648

IG heavy chain V region (clone 2B8) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996

C:Accession: PH1648

R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyl

A:Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1648

A:Molecule type: mRNA

A:Residues: 1-108 <HIL>

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 2e-32;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 97

DB 51 YYADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCA 89

RESULT 25

PH1649

IG heavy chain V region (clone 2E7) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996

C:Accession: PH1649

R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyl

A:Reference number: PH1642; MUID:93301610; PMID:8315388

A:Accession: PH1649

A:Molecule type: mRNA

A:Residues: 1-109 <HIL>

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin



F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 39; DB 2; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 2e-32;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCA 97  
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 Db 51 YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCA 89  
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Search completed: March 15, 2004, 07:39:34  
 Job time : 20 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:37:14 ; Search time 33 Seconds  
(without alignments)  
735.837 Million cell updates/sec

US-09-620-955B-2

Title:   
Perfect score: 115  
Sequence: 1 QVQLSESGGLVPGGSLR.....CARDYFLMGKGLTVTVSS 115

Scoring table: OLIGO

Gapop 60.0 , Capext 60.0

Searched: 809742 seqs, 21153259 residues

Word size : 0

Total number of hits satisfying chosen parameters: 340717

Minimum DB seq length: 0  
Maximum DB seq length: 115

Post-processing: Listing first 100 summaries

Database :

Published Applications: AA\*  
1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pcp.\*  
2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pcp.\*  
3: /cgn2\_6/prodata/1/pubpaa/US05\_NEW\_PUB.pcp.\*  
4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pcp.\*  
5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pcp.\*  
6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pcp.\*  
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8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pcp.\*  
9: /cgn2\_6/prodata/1/pubpaa/US09A\_PUBCOMB.pcp.\*  
10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pcp.\*  
11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pcp.\*  
12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pcp.\*  
13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*  
14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*  
15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pcp.\*  
16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pcp.\*  
17: /cgn2\_6/prodata/1/pubpaa/US40\_NEW\_PUB.pcp.\*  
18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	56.5	115	14	US-10-305-347A-7
2	63	54.8	98	14	US-10-194-975-24
3	63	54.8	98	15	US-10-308-817-64
4	63	54.8	98	15	US-10-032-037B-74
5	63	54.8	98	15	US-10-032-037B-75
6	63	54.8	98	15	US-10-032-037B-76
7	63	54.8	98	15	US-10-029-988B-74
8	63	54.8	98	15	US-10-029-988B-75
9	63	54.8	98	15	US-10-029-988B-76
10	63	54.8	98	15	US-10-032-423A-74
11	63	54.8	98	15	US-10-032-423A-75
12	63	54.8	98	15	US-10-032-423A-76
13	62	53.9	98	14	US-10-194-975-23
14	62	53.9	98	14	US-10-194-975-25
15	62	53.9	98	15	US-10-308-817-63
16	62	53.9	98	15	US-10-308-817-65
17	62	53.9	98	15	US-10-032-037B-80
18	62	53.9	98	15	US-10-029-988B-80
19	62	53.9	98	15	US-10-032-423A-80
20	62	53.9	98	15	US-09-791-153A-63
21	61	53.0	83	14	US-10-078-958-7
22	46	40.0	98	14	US-10-194-975-26
23	46	40.0	98	14	US-10-041-860-4
24	46	40.0	98	14	US-10-041-860-283
25	46	40.0	98	14	US-10-041-860-284
26	46	40.0	98	14	US-10-041-860-307
27	46	40.0	98	14	US-10-041-860-308
28	46	40.0	98	14	US-10-041-860-330
29	46	40.0	98	15	US-10-308-817-66
30	46	40.0	98	15	US-10-032-037B-81
31	46	40.0	98	15	US-10-029-988B-81
32	46	40.0	98	15	US-10-032-423A-81
33	46	40.0	109	15	US-10-309-764-1
34	45	39.1	102	10	US-09-972-656-126
35	41	35.7	98	9	US-09-864-761-44343
36	41	35.7	98	14	US-10-041-860-332
37	40	34.8	97	14	US-10-194-975-29
38	40	34.8	97	14	US-10-194-975-31
39	40	34.8	97	14	US-10-041-860-5
40	40	34.8	97	14	US-10-041-860-277
41	40	34.8	97	15	US-10-308-817-70
42	40	34.8	97	15	US-10-308-817-72
43	40	34.8	97	15	US-10-032-037B-68
44	40	34.8	97	15	US-10-032-037B-69
45	40	34.8	97	15	US-10-029-988B-68
46	40	34.8	97	15	US-10-029-988B-69
47	40	34.8	97	15	US-10-032-423A-68
48	40	34.8	97	15	US-10-032-423A-69
49	40	34.8	102	10	US-09-972-656-123
50	40	34.8	102	10	US-09-972-656-127
51	40	34.8	113	9	US-09-056-160B-11
52	40	34.8	113	11	US-09-795-798-6
53	40	34.8	113	14	US-10-234-671-11
54	39	33.9	96	14	US-10-041-860-278
55	39	33.9	98	9	US-09-822-698A-18
56	39	33.9	98	14	US-10-194-975-22
57	39	33.9	98	14	US-10-125-687-19
58	39	33.9	98	14	US-10-010-942B-10
59	39	33.9	98	15	US-10-308-817-62
60	39	33.9	98	15	US-10-032-037B-77
61	39	33.9	98	15	US-10-029-988B-77
62	39	33.9	98	15	US-10-032-423A-77
63	39	33.9	109	15	US-10-309-764-17
64	39	33.9	112	14	US-10-010-729-15
65	38	33.0	108	14	US-10-026-925-24
66	36	31.3	113	15	US-10-309-764-2
67	35	30.4	98	14	US-10-194-975-30
68	32	27.8	32	9	US-09-855-271-21
69	32	27.8	32	9	US-09-949-558-123
70	32	27.8	32	10	US-09-875-221A-123
71	32	27.8	32	10	US-09-563-222-152
72	31	27.0	32	9	US-09-736-371B-24
73	31	27.0	32	15	US-10-463-442-24
74	29	25.2	30	15	US-10-045-674-91
75	29	25.2	98	14	US-10-194-975-28
76	29	25.2	98	15	US-10-308-817-68
77	29	25.2	98	15	US-10-032-037B-82
78	29	25.2	98	15	US-10-029-988B-82
79	29	25.2	98	15	US-10-032-423A-82
80	29	25.2	114	15	US-10-309-762-145
81	27	23.5	72	14	US-10-026-925-53
82	27	23.5	97	14	US-10-194-975-18
83	27	23.5	97	15	US-10-308-817-58
84	27	23.5	97	15	US-10-032-037B-78
85	27	23.5	97	15	US-10-029-988B-78
86	27	23.5	97	15	US-10-032-423A-78
87	27	23.5	98	13	US-10-066-895-4
88	27	23.5	98	14	US-10-194-975-15
89	27	23.5	98	14	US-10-194-975-15
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92	27	23.5	98	14	US-10-194-975-15
93	27	23.5	98	14	US-10-194-975-15
94	27	23.5	98	14	US-10-194-975-15
95	27	23.5	98	14	US-10-194-975-15
96	27	23.5	98	14	US-10-194-975-15
97	27	23.5	98	14	US-10-194-975-15
98	27	23.5	98	14	US-10-194-975-15
99	27	23.5	98	14	US-10-194-975-15
100	27	23.5	98	14	US-10-194-975-15

89 27 23.5 98 14 US-10-194-975-33  
90 27 23.5 98 15 US-10-308-817-55  
91 27 23.5 98 15 US-10-308-817-71  
92 27 23.5 98 15 US-10-308-817-75  
93 27 23.5 98 15 US-10-032-037B-79  
94 27 23.5 98 15 US-10-032-037B-84  
95 27 23.5 98 15 US-10-032-037B-85  
96 27 23.5 98 15 US-10-029-988B-79  
97 27 23.5 98 15 US-10-029-988B-84  
98 27 23.5 98 15 US-10-029-988B-85  
99 27 23.5 98 15 US-10-032-423A-79  
100 27 23.5 98 15 US-10-032-423A-84

## ALIGNMENTS

RESULT 1  
US-10-305-347A-7  
; Sequence 7, Application US/10305347A  
; Publication No. US20030143603A1  
; GENERAL INFORMATION:  
; APPLICANT: Giles-Komar, Jill  
; APPLICANT: Bernie Scallon  
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CENS005  
; CURRENT APPLICATION NUMBER: US/10/305,347A  
; CURRENT FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver 3.0  
; SEQ ID NO 7  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-305-347A-7

Query Match 56.5%; Score 65; DB 14; Length 115;  
Best Local Similarity 100.0%; Pred. No. 3.9e-52;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVY 95  
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVY 95  
QY 96 CARDR 100  
DB 96 CARDR 100

RESULT 2  
US-10-194-975-24  
; Sequence 24, Application US/10194975  
; Publication No. US20030039649A1  
; GENERAL INFORMATION:  
; APPLICANT: Foote, Jefferson  
; TITLE OF INVENTION: Super Humanized Antibodies  
; FILE REFERENCE: 501231.01  
; CURRENT APPLICATION NUMBER: US/10/194,975  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/305,111  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-194-975-24

Query Match 54.8%; Score 63; DB 14; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.4e-50;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVY 95  
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVY 95  
QY 96 CAR 98  
DB 96 CAR 98

RESULT 3  
US-10-308-817-64  
; Sequence 64, Application US/10308817  
; Publication No. US20030219861A1  
; GENERAL INFORMATION:  
; APPLICANT: Rother, Russell  
; APPLICANT: WJ, Dayang  
; TITLE OF INVENTION: HYBRID ANTIBODIES  
; FILE REFERENCE: 1087-37  
; CURRENT APPLICATION NUMBER: US/10/308,817  
; CURRENT FILING DATE: 2002-12-03  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 64  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: human  
US-10-308-817-64

Query Match 54.8%; Score 63; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.4e-50;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVY 95  
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVY 95  
QY 96 CAR 98  
DB 96 CAR 98

RESULT 4  
US-10-032-037B-74  
; Sequence 74, Application US/10032037B  
; Publication No. US20040001822A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/44  
; CURRENT APPLICATION NUMBER: US/10/032,037B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 74  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-037B-74

Query Match 54.8%; Score 63; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.4e-50;  
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVY 95  
DB 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRAEDTAVY 95  
QY 96 CAR 98  
DB 96 CAR 98

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RESULT 5
US-10-032-037B-75
; Sequence 75, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-75

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
QY 96 CAR 98
Db 96 CAR 98

RESULT 6
US-10-032-037B-76
; Sequence 76, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-76

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
QY 96 CAR 98
Db 96 CAR 98

RESULT 7
US-10-029-988B-74
; Sequence 74, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-74

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
QY 96 CAR 98
Db 96 CAR 98

RESULT 8
US-10-029-988B-75
; Sequence 75, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-75

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
QY 96 CAR 98
Db 96 CAR 98

RESULT 9
US-10-029-988B-76
; Sequence 76, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-76

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
Db 36 WVRQAPGKLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95
QY 96 CAR 98
Db 96 CAR 98
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; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-76

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
Db |||||
Db 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
QY 96 CAR 98
Db |||
Db 96 CAR 98

RESULT 10
US-10-032-423A-74
; Sequence 74, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-74

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
Db |||||
Db 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
QY 96 CAR 98
Db |||
Db 96 CAR 98

RESULT 11
US-10-032-423A-75
; Sequence 75, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-75

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
Db |||||
Db 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
QY 96 CAR 98
Db |||
Db 96 CAR 98

RESULT 12
US-10-032-423A-76
; Sequence 76, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-76

Query Match      54.8%; Score 63; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.4e-50;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
Db |||||
Db 36 WVRQAPGKLEWVAIVSYDGSNKYYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYY 95
QY 96 CAR 98
Db |||
Db 96 CAR 98

RESULT 13
US-10-194-975-23
; Sequence 23, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
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## US-10-194-975-23

Query Match 53.9%; Score 62; DB 14; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWVAVISYDGSNKKYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95  
|||  
Db 36 WVRQAPGKLEWVAVISYDGSNKKYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95  
|||  
Qy 96 CA 97  
|||  
Db 96 CA 97

## RESULT 14

US-10-194-975-25  
; Sequence 25, Application US/10194975  
; Publication No. US20030039649A1  
; GENERAL INFORMATION:  
; APPLICANT: Roore Jefferson  
; TITLE OF INVENTION: Super Humanized Antibodies  
; FILE REFERENCE: 501231.01  
; CURRENT APPLICATION NUMBER: US/10/194,975  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/305,111  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-194-975-25

Query Match 53.9%; Score 62; DB 14; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWVAVISYDGSNKKYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95  
|||  
Db 36 WVRQAPGKLEWVAVISYDGSNKKYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95  
|||  
Qy 96 CA 97  
|||  
Db 96 CA 97

## RESULT 15

US-10-308-817-63  
; Sequence 63, Application US/10308817  
; Publication No. US20030219861A1  
; GENERAL INFORMATION:  
; APPLICANT: Rother, Russell  
; APPLICANT: Wu, Dayang  
; TITLE OF INVENTION: HYBRID ANTIBODIES  
; FILE REFERENCE: 1087-37  
; CURRENT APPLICATION NUMBER: US/10/308,817  
; CURRENT FILING DATE: 2002-12-03  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 63  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: human  
US-10-308-817-63

Query Match 53.9%; Score 62; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWVAVISYDGSNKKYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95  
|||

## Db 36 WVRQAPGKLEWVAVISYDGSNKKYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95

Qy 96 CA 97  
|||  
Db 96 CA 97

## RESULT 16

US-10-308-817-65  
; Sequence 65, Application US/10308817  
; Publication No. US20030219861A1  
; GENERAL INFORMATION:  
; APPLICANT: Rother, Russell  
; APPLICANT: Wu, Dayang  
; TITLE OF INVENTION: HYBRID ANTIBODIES  
; FILE REFERENCE: 1087-37  
; CURRENT APPLICATION NUMBER: US/10/308,817  
; CURRENT FILING DATE: 2002-12-03  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 65  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: human  
US-10-308-817-65

Query Match 53.9%; Score 62; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWVAVISYDGSNKKYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95  
|||  
Db 36 WVRQAPGKLEWVAVISYDGSNKKYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95  
|||  
Qy 96 CA 97  
|||  
Db 96 CA 97

## RESULT 17

US-10-032-037B-80  
; Sequence 80, Application US/10032037B  
; Publication No. US20040001822A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/44  
; CURRENT APPLICATION NUMBER: US/10/032,037B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 80  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-037B-80

Query Match 53.9%; Score 62; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 WVRQAPGKLEWVAVISYDGSNKKYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95  
|||  
Db 36 WVRQAPGKLEWVAVISYDGSNKKYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYY 95  
|||  
Qy 96 CA 97  
|||  
Db 96 CA 97

## RESULT 18

US-10-029-988B-80  
; Sequence 80, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029,988B  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 80  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-988B-80

Query Match 53.9%; Score 62; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 36 WYRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYY 95  
DB 36 WYRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYY 95  
QY 96 CA 97  
DB 96 CA 97

## RESULT 19

US-10-032-423A-80  
; Sequence 80, Application US/10032423A  
; Publication No. US20040002450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/45  
; CURRENT APPLICATION NUMBER: US/10/032,423A  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 80  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-423A-80

Query Match 53.9%; Score 62; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 36 WYRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYY 95  
DB 36 WYRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYY 95  
QY 96 CA 97  
DB 96 CA 97

## RESULT 20

US-09-791-153A-63  
; Sequence 63, Application US/09791153A  
; Publication No. US20030103978A1  
; GENERAL INFORMATION:

; APPLICANT: Deshpande, Rajendra  
; APPLICANT: Hitz, Anna  
; APPLICANT: Boyle, William  
; APPLICANT: Sullivan, John  
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN  
; FILE REFERENCE: A-633A  
; CURRENT APPLICATION NUMBER: US/09/791,153A  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 09/511,139  
; PRIOR FILING DATE: 2000-02-23  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 63  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-153A-63

Query Match 53.9%; Score 62; DB 10; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2.2e-49;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 36 WYRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYY 95  
DB 36 WYRQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYY 95  
QY 96 CA 97  
DB 96 CA 97

## RESULT 21

US-10-078-958-7  
; Sequence 7, Application US/10078958  
; Publication No. US20030070185A1  
; GENERAL INFORMATION:  
; APPLICANT: JAKOBOVITS, AYA  
; APPLICANT: KUCHERLAPATI, RAJU  
; APPLICANT: KLAPHOLZ, SUSAN  
; APPLICANT: MENDEZ, MICHAEL J.  
; APPLICANT: GREEN, LARRY  
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING  
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED  
; FILE REFERENCE: CELL 4.18 CON  
; CURRENT APPLICATION NUMBER: US/10/078,958  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 08/759,620  
; PRIOR FILING DATE: 1996-12-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 83  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (22)  
; OTHER INFORMATION: Variable amino acid  
US-10-078-958-7

Query Match 53.0%; Score 61; DB 14; Length 83;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 38 RQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCA 97  
DB 23 RQAPGKLEWAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCA 82  
QY 98 R 98  
DB 83 R 83

```
RESULT 22
US-10-194-975-26
; Sequence 26, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Fooce, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent version 3.1
; SEQ ID NO 26
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-26

Query Match      40.0%; Score 46; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 98
Db 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 98

RESULT 23
US-10-041-860-4
; Sequence 4, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-4

Query Match      40.0%; Score 46; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 98
Db 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 98

RESULT 24
US-10-041-860-283
; Sequence 283, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-283

Query Match      40.0%; Score 46; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 98
Db 53 YDGSNKYYADSVKGRFTISRDNKNTLYLQMSLRRAEDTAVYYCAR 98

Search completed: March 15, 2004, 07:40:55
Job time : 33 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:29:28 ; Search time 39 Seconds  
(without alignments)  
930.374 Million cell updates/sec

Title: US-09-620-955B-2

Perfect score: 115

Sequence: 1 QVLOESGGLVQPGSLRL.....CARDRYFLWGRGLIVTSS 115

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 217408

Minimum DB seq length: 0

Maximum DB seq length: 115

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 25:

- 1: sp\_archaea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_human:
- 5: sp\_invertebrate:
- 6: sp\_mammal:
- 7: sp\_mhc:
- 8: sp\_organelle:
- 9: sp\_phage:
- 10: sp\_plant:
- 11: sp\_rodent:
- 12: sp\_virus:
- 13: sp\_vertebrate:
- 14: sp\_unclassified:
- 15: sp\_rvirus:
- 16: sp\_bacteriap:
- 17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	39.1	113	4	Q9UL90
2	40	34.8	112	4	Q9UGP3
3	27	23.5	95	4	Q9ULB6
4	20	17.4	112	4	Q9HCC1
5	15	13.0	104	4	Q9UL87
6	11	9.6	64	11	Q9UL750
7	10	8.7	15	11	Q9QV16
8	8	7.0	109	11	Q9JLB5
9	8	7.0	109	11	Q9JL75
10	7	6.1	102	11	Q9JL79
11	7	6.1	110	11	Q9JL63
12	7	6.1	110	11	Q9JL77
13	7	6.1	111	11	Q9D9B8
14	7	6.1	114	11	Q9JLB1
15	6	5.2	16	4	Q9UC53
16	6	5.2	29	12	Q9LHB1

17	5.2	38	4	015224	O15224 homo sapien
18	5.2	44	6	Q8WNG3	Q8WNG3 pan troglod
19	5.2	58	16	Q8EV56	Q8EV56 mycoplasma
20	5.2	66	12	Q8QQ63	Q8QQ63 camelpox vi
21	5.2	66	12	Q9JFD1	Q9JFD1 vaccinia vi
22	5.2	67	8	Q7YN75	Q7YN75 eimeria ten
23	5.2	70	17	Q8TQ32	Q8TQ32 methanosarc
24	5.2	72	2	Q8GB47	Q8GB47 clostridium
25	5.2	73	16	Q7UZ17	Q7UZ17 rhodospirill
26	5.2	74	10	Q8H8Q8	Q8H8Q8 oryza sativ
27	5.2	78	16	Q8WB6	Q8WB6 streptococc
28	5.2	83	17	Q8THX0	Q8THX0 methanosarc
29	5.2	85	8	Q8MDL1	Q8MDL1 packera can
30	5.2	91	10	Q8HOY6	Q8HOY6 arabidopsis
31	5.2	92	10	Q8L7G7	Q8L7G7 arabidopsis
32	5.2	96	8	Q8MDN9	Q8MDN9 erechthites
33	5.2	104	16	Q31480	Q31480 bacillus su
34	5.2	105	5	Q819M3	Q819M3 chlamys far
35	5.2	105	8	Q8MDL5	Q8MDL5 senecio ang
36	5.2	106	8	Q9MFF2	Q9MFF2 beta vulgar
37	5.2	106	8	Q8MDK9	Q8MDK9 othonna cap
38	5.2	106	8	Q8MDM2	Q8MDM2 senecio ina
39	5.2	106	8	Q8HU25	Q8HU25 zoster mar
40	5.2	106	8	Q8HU24	Q8HU24 zoster jap
41	5.2	106	8	Q8HU23	Q8HU23 zoster nol
42	5.2	106	8	Q8HU22	Q8HU22 zoster nov
43	5.2	106	8	Q8HU21	Q8HU21 zoster cap
44	5.2	106	8	Q8HU20	Q8HU20 zoster mue
45	5.2	106	8	Q8HBN3	Q8HBN3 bradyrhizob
46	5.2	106	16	Q89BN3	Q89BN3 bombax mori
47	5.2	107	5	Q8BLD5	Q8BLD5 senecio cin
48	5.2	107	8	Q8MDL8	Q8MDL8 senecio cin
49	5.2	107	12	Q12379	Q12379 marek's dis
50	5.2	108	8	Q8MDM0	Q8MDM0 senecio ere
51	5.2	108	8	Q8MDK5	Q8MDK5 dendrosenec
52	5.2	108	8	Q8MDQ4	Q8MDQ4 senecio amb
53	5.2	108	15	Q998Z1	Q998Z1 human immun
54	5.2	108	16	Q7VJB1	Q7VJB1 helicobacte
55	5.2	109	5	Q8T4C7	Q8T4C7 drosophila
56	5.2	109	8	Q8MDK3	Q8MDK3 blennosperm
57	5.2	109	8	Q8MDM7	Q8MDM7 senecio pal
58	5.2	109	8	Q8MDP8	Q8MDP8 senecio chr
59	5.2	109	8	Q8MDL0	Q8MDL0 packera aur
60	5.2	109	8	Q8MDP9	Q8MDP9 senecio dor
61	5.2	110	8	Q8MDK6	Q8MDK6 emilia cocc
62	5.2	111	8	Q8MDN3	Q8MDN3 senecio squ
63	5.2	111	8	Q8MDP5	Q8MDP5 pseudosynox
64	5.2	111	8	Q8MDQ5	Q8MDQ5 synotis neg
65	5.2	111	8	Q8MDQ3	Q8MDQ3 senecio pan
66	5.2	111	8	Q8MDK8	Q8MDK8 kleinia ner
67	5.2	111	8	Q8MDM4	Q8MDM4 senecio lau
68	5.2	111	8	Q8MDK7	Q8MDK7 euryops pec
69	5.2	111	8	Q8MDN0	Q8MDN0 senecio ser
70	5.2	111	8	Q8MDN7	Q8MDN7 arthenschth
71	5.2	111	8	Q8MDP2	Q8MDP2 lorthowea i
72	5.2	111	8	Q8MDM9	Q8MDM9 senecio sca
73	5.2	111	8	Q8MDP0	Q8MDP0 gynoxys sou
74	5.2	111	16	Q8MDP4	Q8MDP4 phaneroglos
75	5.2	111	16	Q88F31	Q88F31 pseudomonas
76	5.2	112	8	Q8MDL4	Q8MDL4 senecio ane
77	5.2	112	8	Q8MDL7	Q8MDL7 senecio art
78	5.2	112	8	Q8MDL3	Q8MDL3 senecio ado
79	5.2	112	8	Q8MDM6	Q8MDM6 senecio nem
80	5.2	112	8	Q8MDQ0	Q8MDQ0 senecio car
81	5.2	112	8	Q8MDN4	Q8MDN4 senecio vis
82	5.2	112	8	Q8MDM8	Q8MDM8 senecio row
83	5.2	112	8	Q8MDN1	Q8MDN1 senecio sub
84	5.2	113	8	Q8VDO1	Q8VDO1 senecio min
85	5.2	114	2	Q8VW89	Q8VW89 terrabacter
86	5.2	114	8	Q8MDM5	Q8MDM5 senecio med
87	5.2	114	8	Q8VDN2	Q8VDN2 senecio syl
88	5.2	114	8	Q8VDM1	Q8VDM1 senecio eru
89	5.2	114	8	Q8MDL6	Q8MDL6 senecio aqu

90 6 5.2 114 12 Q911W9  
91 6 5.2 114 12 Q911W7  
92 6 5.2 114 12 Q911W8  
93 6 5.2 114 12 Q911W6  
94 6 5.2 114 12 Q911W5  
95 6 5.2 114 15 P88783  
96 6 5.2 114 16 Q9JWD0  
97 6 5.2 115 8 Q9GLH0  
98 6 5.2 115 8 Q9G9Y9  
99 6 5.2 115 8 Q93905  
100 6 5.2 115 8 Q953K0

Q911W9 human polio  
Q911W7 human polio  
Q911W8 human polio  
Q911W6 human polio  
Q911W5 human polio  
P88783 human immun  
Q9JWD0 neisseria m  
Q9GLH0 eulemur ful  
Q9G9Y9 eulemur ful  
Q93905 myoxus glis  
Q953K0 ochotona co

## ALIGNMENTS

RESULT 1  
Q9UL90 PRELIMINARY; PRT; 113 AA.  
AC Q9UL90;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetuses";  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
DR EMBL; AF035024; AAD56260.1; --  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS08335; IG LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 113  
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;  
Query Match 39.1%; Score 45; DB 4; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2.5e-39;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 53 YDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVYCA 97  
Db 53 YDGSNKYVADSVKGRFTISRDNKNTLYLQWNSLRADTAVYCA 97  
RESULT 2  
Q9UGP3 PRELIMINARY; PRT; 112 AA.  
AC Q9UGP3;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Immunoglobulin heavy chain (Fragment)  
DE IGH.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zafiroopoulos A., Kandilogianaki M., Dahlenborg C., Borrebaeck C.A.K.,  
Query Match 23.5%; Score 27; DB 4; Length 95;  
Best Local Similarity 100.0%; Pred. No. 2.2e-20;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32  
Db 5 ESGGGLVQPGGSLRLSCAASGFTFSY 31  
RESULT 4  
Q9HCC1 PRELIMINARY; PRT; 112 AA.  
AC Q9HCC1;  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Single chain Fv (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RA Krambovitis E.;  
RT "Induction of somatic mutations in human B cells by in vitro  
immunization";  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ132560; CAB65078.1; --  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS08335; IG LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 112  
SQ SEQUENCE 112 AA; 12226 MW; 0A1F17082C7A8CE3 CRC64;  
Query Match 34.8%; Score 40; DB 4; Length 112;  
Best Local Similarity 100.0%; Pred. No. 4.7e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 60 YADSVKGRFTISRDNKNTLYLQWNSLRADTAVYCA 99  
Db 43 YADSVKGRFTISRDNKNTLYLQWNSLRADTAVYCA 82  
RESULT 3  
Q9ULB6 PRELIMINARY; PRT; 95 AA.  
AC Q9ULB6;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Immunoglobulin heavy chain (Fragment)  
DE VH.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tange Y., Kayano H.;  
RT "Human VH gene sequence";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB035268; BAA87067.1; --  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS08335; IG LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 95  
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;  
Query Match 23.5%; Score 27; DB 4; Length 95;  
Best Local Similarity 100.0%; Pred. No. 2.2e-20;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 ESGGGLVQPGGSLRLSCAASGFTFSY 32  
Db 5 ESGGGLVQPGGSLRLSCAASGFTFSY 31  
RESULT 4  
Q9HCC1 PRELIMINARY; PRT; 112 AA.  
AC Q9HCC1;  
DT 01-MAR-2001 (TRENBLrel. 16, Created)  
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Single chain Fv (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme: Isolation from a
RL human synthetic phage display library and characterization.";
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF000047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24FLA45EC3B84788 CRC64;

Query Match 17.4%; Score 20; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 6.3e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 LXIQMNSLRAEDTAVYICAR 98
DB 79 LXIQMNSLRAEDTAVYICAR 98
|||||
RESULT 5
Q9UL87 PRELIMINARY; PRT; 104 AA.
ID Q9UL87
AC Q9UL87;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035027; AAD56263.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF000047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;

Query Match 13.0%; Score 15; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 YADSVKGRFTISRDN 74
DB 39 YADSVKGRFTISRDN 53
|||||
RESULT 6
Q61750 PRELIMINARY; PRT; 64 AA.
ID Q61750
AC Q61750;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE JH-Cdelta locus (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=92017847; PubMed=1922069;
RA Owens J.D.Jr., Finkelman F.D., Mountz J.D., Mushinski J.F.;
RT "Nonhomologous recombination at sites within the mouse JH-cdelta locus
RL Mol. Cell. Biol. 11:5660-5670(1991).
DR EMBL; M64568; AAA39341.1; -.
DR PIR; I77394; I77394.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 64 AA; 7594 MW; FE83625079AC2F28 CRC64;

Query Match 9.6%; Score 11; DB 11; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 SVKGRFTISRDN 73
DB 23 SVKGRFTISRDN 33
|||||
RESULT 7
Q9QV16 PRELIMINARY; PRT; 15 AA.
ID Q9QV16
AC Q9QV16;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Prolactin-binding protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=95094032; PubMed=8000909;
RA Cohen H., Cohen O., Gagnon J.;
RT "Serum prolactin-binding protein (PRL-BP) of human and rat are
RT identified as IGF.";
RL C. R. Acad. Sci., III, Sci. Vie 317:293-298(1994).
SQ SEQUENCE 15 AA; 1469 MW; 35ED2512FF3FA369 CRC64;

Query Match 8.7%; Score 10; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPG 15
DB 6 ESGGGLVQPG 15
|||||
RESULT 8
Q9JL85 PRELIMINARY; PRT; 109 AA.
ID Q9JL85
AC Q9JL85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206021; AAF69319.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 109 AA; 11944 MW; DF5615FE6CEDA8E CRC64;

Query Match 7.0%; Score 8; DB 11; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 EDTAVYVC 96
DB 81 EDTAVYVC 88

RESULT 9
Q9JL75 PRELIMINARY; PRT; 109 AA.
AC Q9JL75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-mycosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206031; AAF69329.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 109 AA; 12118 MW; FF5E441B5F936A6 CRC64;

Query Match 7.0%; Score 8; DB 11; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 AVYVCARD 99
DB 83 AVYVCARD 90

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RESULT 10
Q9JL79 PRELIMINARY; PRT; 102 AA.
AC Q9JL79;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-mycosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A.CA;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206027; AAF69325.1; -.
DR HSSP; P01772; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 102 AA; 11543 MW; E590C292093F6711 CRC64;

Query Match 6.1%; Score 7; DB 11; Length 102;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 QAPGKGL 45
DB 24 QAPGKGL 30

RESULT 11
Q9JL83 PRELIMINARY; PRT; 110 AA.
AC Q9JL83;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-mycosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206023; AAF69321.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1

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FT NON_TER 110 110
SQ SEQUENCE 110 AA; 12052 MW; 84EGF2AD219AF95E CRC64;

Query Match
Best Local Similarity 6.1%; Score 7; DB 11; Length 110;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 GTLVTVS 114
DB 103 GTLVTVS 109

RESULT 12
Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DEA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206029; AAF69327.1; -.
DR FIC; F33932; F33932.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FBS862C9AF CRC64;

Query Match
Best Local Similarity 6.1%; Score 7; DB 11; Length 110;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 AVYYCAR 98
DB 84 AVYYCAR 90

RESULT 13
Q9D9B8 PRELIMINARY; PRT; 111 AA.
AC Q9D9B8
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adult male testis cDNA, RIKEN full-length enriched library,
DE clone:1700110b11, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.
RA "Functional annotation of a full-length mouse cDNA collection.";
ET Nature 409:685-690(2001).
RL EMBL; AK007163; BAB24877.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;

Query Match
Best Local Similarity 6.1%; Score 7; DB 11; Length 111;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 PGKGLEW 47
DB 47 PGKGLEW 53

RESULT 14
Q9JL81 PRELIMINARY; PRT; 114 AA.
AC Q9JL81
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206025; AAF69323.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;

Query Match
Best Local Similarity 6.1%; Score 7; DB 11; Length 114;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 92 AVYYCAR 98  
Db 84 AVYYCAR 90

RESULT 15  
Q9UC53 PRELIMINARY; PRT; 16 AA.  
AC Q9UC53  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
DE 77 kDa SPONTANEOUS RECURRENT ABORTION-associated human embryonic antigen/IGVHIII homolog (Fragment).  
DE Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=96033130; PubMed=8582963;  
RA Shiraishi Y., Shiraishi Y., Yamamoto D., Hasegawa T., Kitamura W.,  
RA Miki S., Tanaka T., Suzuki T., Soma H.;  
RT "Diagnostic relevance of abortion-associated human embryonic antigen  
RT expressed on the cell surface of tumour promoter-treated Bloom syndrome  
RL Hum. Reprod. 10:1694-1701(1995).  
SQ SEQUENCE 16 AA; 1626 MW; C9C5ED2512FF3FB9 CRC64;

Query Match 5.2%; Score 6; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GLVQPG 15  
Db 10 GLVQPG 15

RESULT 16  
Q91HB1 PRELIMINARY; PRT; 29 AA.  
AC Q91HB1  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Porcine circovirus type 2.  
OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
OX NCBI\_TaxID=85708;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shengbo C., Huanhun C.;  
RT "Cloning and sequence analysis of the genome of Porcine Circovirus  
RT type 2 isolated from pig with PMWS in China."  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY035820; AAK60466.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 29 AA; 3223 MW; 87D7DC201205CEC7 CRC64;

Query Match 5.2%; Score 6; DB 12; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GGSRLR 20  
Db 11 GGSRLR 16

RESULT 17  
O15224 PRELIMINARY; PRT; 38 AA.  
ID O15224  
AC O15224;

DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE CDR3-IGM (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Follicle centre lymphoma;  
RX MEDLINE=98261457; PubMed=9596678;  
RA Ottensmeier C.H., Thompson A.R., Zhu D., Wilkins B.S.,  
RA Swettenham J.W., Stevenson F.K.;  
RT "Analysis of VH genes in follicular and diffuse lymphoma shows ongoing  
RT somatic mutation and multiple isotype transcripts in early disease  
RT with changes during disease progression."  
RL Blood 91:4292-4299(1998).  
DR EMBL; AJ001411; CAA04746.1; -.  
DR HSP; P01810; 2PBJ.  
DR InterPro; IPR007110; IG-like.  
FT NON\_TER 1  
FT NON\_TER 38  
SQ SEQUENCE 38 AA; 4365 MW; C68B5B68A32ECD5 CRC64;

Query Match 5.2%; Score 6; DB 4; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 LVTSS 115  
Db 22 LVTSS 27

RESULT 18  
Q8WNG3 PRELIMINARY; PRT; 44 AA.  
AC Q8WNG3  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE NPIP-like protein (Fragment).  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=LCR15a duplication region;  
RX MEDLINE=21470411; PubMed=11586358;  
RA Johnson M.E., Viggiano L., Bailey J.A., Abdul-Rauf M., Goodwin G.,  
RA Rocchi M., Eichler E.E.;  
RT "Positive selection of a gene family during the emergence of humans  
RT and African apes."  
RL Nature 413:514-519(2001).  
DR EMBL; AF364277; AAL50491.1; -.  
FT NON\_TER 1  
FT NON\_TER 44  
SQ SEQUENCE 44 AA; 4985 MW; A875B2DA8DB7D3C3 CRC64;

Query Match 5.2%; Score 6; DB 6; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GGSRLR 20  
Db 16 GGSRLR 21

RESULT 19  
Q8EV56 PRELIMINARY; PRT; 58 AA.  
ID Q8EV56  
AC Q8EV56;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN MYEF7115.  
 OS Mycoplasma penetrans.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=28227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HF-2;  
 RX MEDLINE=22354719; PubMed=12466555;  
 RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,  
 RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;  
 RT "The complete genomic sequence of Mycoplasma penetrans, an  
 RT intracellular bacterial pathogen in humans.";  
 RL Nucleic Acids Res. 30:5293-5300(2002).  
 DR EMBL; AP04173; BAC44504.1;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 58 AA; 6743 MW; 82751A7819556B18 CRC64;  
  
 Query Match 5.2%; Score 6; DB 16; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 53 YGGSNK 58  
 Db 41 YDGSNK 46  
 |||||  
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 RESULT 20  
 ID Q8Q063 PRELIMINARY; PRT; 66 AA.  
 AC Q8Q063  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DE Orthopoxvirus.  
 DE CWP60.5L.  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 GN CWP60.5L.  
 OS Camelopox virus (strain CP-1).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxID=203174;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CWS;  
 RX PubMed=11907336;  
 RA Gubser C., Smith G.L.;  
 RT "The sequence of camelopox virus shows it is most closely related to  
 RT variola virus, the cause of smallpox.";  
 RL J. Gen. Virol. 83:855-872(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CWS;  
 RA Gubser C., Smith G.L.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY009089; AAG37525.1;  
 SQ SEQUENCE 66 AA; 7633 MW; 0B9B3A120088110A CRC64;  
  
 Query Match 5.2%; Score 6; DB 12; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 27 FTFSSY 32  
 Db 38 FTFSSY 43  
 |||||  
 |||||  
  
 RESULT 21  
 ID Q9JFD1 PRELIMINARY; PRT; 66 AA.  
 AC Q9JFD1  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Vaccinia virus (strain Tian Tan).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OX NCBI\_TaxID=10253;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Tian Tan;  
 RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,  
 RA Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;  
 RT "Complete genomic sequence of vaccinia virus (Tian Tan strain).";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF095689; AAF33921.1;  
 KW Hypothetical protein.  
 SQ SEQUENCE 66 AA; 7618 MW; 0D460CCFB088110A CRC64;  
  
 Query Match 5.2%; Score 6; DB 12; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 27 FTFSSY 32  
 Db 38 FTFSSY 43  
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 RESULT 22  
 ID Q7YN75 PRELIMINARY; PRT; 67 AA.  
 AC Q7YN75  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DE Ribosomal protein S17.  
 OS Eimeria tenella.  
 OC Chloroplast.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;  
 OC Eimeria.  
 OX NCBI\_TaxID=5802;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cai X., Zhu G.;  
 RT "Eimeria tenella plastid genome complete sequence.";  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY217738; AA040228.1;  
 SQ SEQUENCE 67 AA; 8291 MW; CECADFCE65621A6 CRC64;  
  
 Query Match 5.2%; Score 6; DB 8; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 56 SNKYA 61  
 Db 11 SNKYA 16  
 |||||  
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 RESULT 23  
 ID Q8TQ32 PRELIMINARY; PRT; 70 AA.  
 AC Q8TQ32  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DE Predicted protein.  
 GN MAL720.  
 OS Methanosarcina acetivorans.  
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;  
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2214;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=C2A / ATCC 35395 / DSM 2834;  
RX MEDLINE=21929760; PubMed=1932238;  
RA Galagan J.E., Nussbaum C., Roy A., Endrizzi M.G., Macdonald P.,  
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Athoor D., Brown A.,  
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,  
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,  
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,  
RA Hederich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,  
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,  
RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,  
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,  
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,  
RA Metcalf W.W., Birren B.;  
RT "The genome of *Methanosaeta* acetivorans reveals extensive metabolic  
RT and physiological diversity.";  
RL Genome Res. 12:532-542(2002).  
DR EMBL; AE010846; AAM05127.1; ...  
DR InterPro; IPR000437; Prok\_LipoProt S.  
DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
KW Complete proteome.  
SQ SEQUENCE 70 AA; 7976 MW; 457FDF69DEAA054A CRC64;  
  
Query Match 5.2%; Score 6; DB 17; Length 70;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 LQESGG 9  
Db 46 LQESGG 51  
|||||

RESULT 24  
Q8GB47 PRELIMINARY; PRT; 72 AA.  
AC Q8GB47;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Circularin A precursor.  
GN CIRA.  
OS Clostridium beijerinckii (Clostridium MP).  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1520;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 25752;  
RA Kempman R.A., Kuipers A., Karsens H., Nauta A., Kuipers O.P.,  
RA Kok J.;  
RT "Identification and Characterization of Two Novel Clostridial  
RT Bacteriocins, Circularin A and Closticin 574.";  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 25752;  
RA Kempman R.A., Jonker M., Nauta A., Kuipers O.P., Kok J.;  
RT "Functional analysis of the gene cluster involved in circularin A  
RT production by Clostridium beijerinckii ATCC 25752.";  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY164463; AAN86036.1; ...  
DR EMBL; AJ566621; CAD97580.1; ...  
FT CHAIN 4 72 CIRCULARIN A.  
SQ SEQUENCE 72 AA; 7181 MW; 33CB17A2C10A5FA6 CRC64;  
  
Query Match 5.2%; Score 6; DB 2; Length 72;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 108 GTLTV 113  
Db 26 GTLTV 31  
|||||

RESULT 25  
Q7UZ17 PRELIMINARY; PRT; 73 AA.  
AC Q7UZ17;  
DT 01-OCT-2003 (TReMBLrel. 25, Created)  
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN RB257.  
OS Rhodopirellula baltica.  
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
OC Planctomycetaceae; Pirellula.  
OX NCBI\_TaxID=117;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1;  
RX MEDLINE=22735913; PubMed=12835416;  
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,  
RA Schlesner H., Amann R., Reinhardt R.;  
RT "Complete genome sequence of the marine planctomycete *Pirellula* sp.  
RT strain 1.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).  
DR EMBL; BX294133; CAD71469.1; ...  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 73 AA; 7775 MW; 18850A06C941FA60 CRC64;  
  
Query Match 5.2%; Score 6; DB 16; Length 73;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 ESGGGL 11  
Db 50 ESGGGL 55  
|||||

Search completed: March 15, 2004, 07:39:06  
Job time : 44 secs



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OM protein - protein search, using sw model

Run on: March 15, 2004, 07:29:28 ; Search time 17 Seconds  
(without alignments)  
352.239 Million cell updates/sec

Title: US-09-620-955b-2  
Perfect score: 115  
Sequence: 1 QVQLQESGGGLVQPGGSLRL.....CARDRYFDLWGRGLVTVSS 115

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19291

Minimum DB seq length: 0  
Maximum DB seq length: 115

Post-processing: Listing first 100 summaries

Database : SwissProt\_42.1

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	21.7	115	1 HV3D HUMAN	P01765 homo sapien
2	19	16.5	114	1 HV01 CANFA	P01784 canis faml
3	17	14.8	115	1 HV3S HUMAN	P01780 homo sapien
4	16	13.9	115	1 HV3F HUMAN	P01767 homo sapien
5	14	12.2	114	1 HV3B HUMAN	P01763 homo sapien
6	13	11.3	97	1 HV56 MOUSE	P18527 mus musculus
7	13	11.3	98	1 HV57 MOUSE	P18528 mus musculus
8	12	10.4	111	1 HV35 MOUSE	P01804 mus musculus
9	12	10.4	113	1 HV27 MOUSE	P01796 mus musculus
10	12	10.4	113	1 HV28 MOUSE	P01797 mus musculus
11	12	10.4	113	1 HV29 MOUSE	P01798 mus musculus
12	12	10.4	113	1 HV30 MOUSE	P01799 mus musculus
13	12	10.4	113	1 HV31 MOUSE	P01800 mus musculus
14	12	10.4	115	1 HV32 MOUSE	P01801 mus musculus
15	12	10.4	115	1 HV33 MOUSE	P01802 mus musculus
16	11	9.6	113	1 HV34 MOUSE	P01803 mus musculus
17	7	6.1	113	1 HV47 MOUSE	P01823 mus musculus
18	7	6.1	114	1 HV00 MOUSE	P01741 mus musculus
19	7	6.1	114	1 HV2A RABIT	P01827 oryctolagus
20	7	6.1	115	1 HV44 MOUSE	P01820 mus musculus
21	6	5.2	66	1 HV4D VACCV	P20556 vaccinia vi
22	6	5.2	67	1 RPOZ BACSU	O35011 bacillus su
23	6	5.2	68	1 RPOZ BACHD	O9K9Y3 bacillus ha
24	6	5.2	93	1 NEUI STRCA	P15444 struthio ca
25	6	5.2	102	1 YG81 WOLSU	O34247 wolinnella s
26	6	5.2	106	1 YF81 ARCFU	O28691 archaeglob
27	6	5.2	107	1 Y231 RHIME	O92ax1 rhizobium m
28	6	5.2	107	1 YJ09 BRUME	O8yeg9 bruceella me
29	6	5.2	111	1 Y6G8 PSEPK	O88f31 pseudomonas
30	6	5.2	115	1 NU3M DUGDU	O8w9m9 dugong dugo
31	6	5.2	115	1 NU3M RABIT	O79434 oryctolagus
32	5	4.3	27	1 GRP CHICK	P01295 gallus gall
33	5	4.3	40	1 R36Z_STRCO	Q93jh3 streptomyce

#### ALIGNMENTS

RESULT 1

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HV3D HUMAN
ID HV3D HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78005528; PubMed=409716;
RA Wang A.-C.; Wang I.-Y.; Fudenberg H.H.;
RT "Immunoglobulin structure and Genetics. Identity between variable
regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC -!- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
IDENTICAL.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02048; H3HUTL.
DR HSSP; P01772; 2F84.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 108 IG-LIKE.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 21.7%; Score 25; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.6e-19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQGGSLRLSCAASGFTFS 30
DB 6 ESGGGLVQGGSLRLSCAASGFTFS 30

RESULT 2
HV01 CANFA
ID HV01 CANFA STANDARD; PRT; 114 AA.
AC P01784;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region GOW.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=77242269; PubMed=407924;
RA Wasserman R.L.; Capra J.D.;
RT "Primary structure of the variable regions of two canine
immunoglobulin heavy chains.";
RL Biochemistry 16:3160-3168(1977).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02067; AVDGM.
DR HSSP; P01772; 2F84.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.

HV3D HUMAN
ID HV3D HUMAN STANDARD; PRT; 115 AA.
AC P01780;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region JON.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74142702; PubMed=4522793;
RA Capra J.D.; Kehoe J.M.;
RT "Variable region sequences of five human immunoglobulin heavy chains
of the VH3 subgroup: definitive identification of four heavy chain
hypervariable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG3 MYELOMA
PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02063; G3HUUN.
DR HSSP; P01772; 2F84.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12563 MW; 68B668E531C12514 CRC64;

Query Match 14.8%; Score 17; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PGGSRLSLSCAASGFTFS 30
DB 14 PGGSRLSLSCAASGFTFS 30

RESULT 4
HV3F HUMAN
ID HV3F HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=78137069; PubMed=416441;  
RA Torano A., Putnam F.W.;  
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human  
IG2 immunoglobulin of the A2m (2) allotype.";  
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).  
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C  
REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC PIR; A02050; A2HUBU.  
DR HSP; P01789; IMCP.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-Like.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 111 IG-LIKE.  
FT NON\_TER 115 115  
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;  
  
Query Match 13.9%; Score 16; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 1.4e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 13 QPGGSLRLSCAASGFT 28  
DB 13 QPGGSLRLSCAASGFT 28  
[1]|||||  
  
RESULT 5  
HV3B\_HUMAN STANDARD; PRT; 114 AA.  
ID HV3B\_HUMAN  
AC P01763;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-III region WEA.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83273707; PubMed=6410398;  
RA Goni F., Frangione B.;  
RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
(protein WEA) with antibody activity against 3,4-pyruvylated  
galactose in Klebsiella polysaccharides K30 and K33.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY  
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH  
WALDENSTROM'S MACROGLOBULINEMIA.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC PIR; A02046; M3HUWE.  
DR HSP; P01772; 2PB4.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-Like.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
FT DOMAIN 1 112 IG-LIKE.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT NON\_TER 114 114  
SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;  
  
Query Match 12.2%; Score 14; DB 1; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 59 YYADSVKGRFTISR 72  
DB 59 YYADSVKGRFTISR 72  
[1]|||||  
  
RESULT 6  
HV56\_MOUSE STANDARD; PRT; 97 AA.  
ID HV56\_MOUSE  
AC P18527;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 914.  
OS Mus musculus (Mouse);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/cJ;  
RA MEDLINE=89279149; PubMed=2499654;  
RX Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during  
the primary immune response.";  
RL J. Exp. Med. 169:2007-2019(1989).  
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; J0504; HVMS91.  
DR HSP; P01810; 2FBJ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 97  
FT NON\_TER 97 97  
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;  
  
Query Match 11.3%; Score 13; DB 1; Length 97;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 20 LSCAASGFTFSY 32  
DB 20 LSCAASGFTFSY 32  
[1]|||||  
  
RESULT 7  
HV57\_MOUSE STANDARD; PRT; 98 AA.  
ID HV57\_MOUSE  
AC P18528;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 6.96.  
OS Mus musculus (Mouse);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/cJ;  
RA MEDLINE=89279149; PubMed=2499654;  
RX Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during

```
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE HV7183 SUBFAMILY.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; JTC0501; HVMS96.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG-LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 >98 IG-LIKE.
FT NON TER 98
FT SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 11.3%; Score 13; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 DSVKGRFTISRDN 74
DB 62 DSVKGRFTISRDN 74

RESULT 8
HV35_MOUSE STANDARD; PRT; 111 AA.
AC P01804;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region HPC76 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8101397; PubMed=6251474;
RA Bernard O., Gough N.M.;
RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
between translocated VH and mu constant regions genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C
REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE
CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02074; MHMS76.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG-LIKE; 1.
DR Immunoglobulin V region.
FT NON TER 1
FT DOMAIN <1 110 IG-LIKE.
FT NON TER 111
FT SEQUENCE 111 AA; 12304 MW; 0EDE98EC7348056A CRC64;

Query Match 10.4%; Score 12; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 1 ESGGGLVQPGGS 12

RESULT 9
HV27_MOUSE STANDARD; PRT; 113 AA.
ID HV27_MOUSE
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; B93818; AVMS61.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG-LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113 113
FT SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;

Query Match 10.4%; Score 12; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 6 ESGGGLVQPGGS 17

RESULT 10
HV28_MOUSE STANDARD; PRT; 113 AA.
ID HV28_MOUSE
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; B93818; AVMS61.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG-LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113 98
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```
FT NON TER 113
SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;

Query Match 10.4%; Score 12; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 6 ESGGGLVQPGGS 17

RESULT 11
HV29 MOUSE
ID HV29 MOUSE STANDARD; PRT; 113 AA.
AC P01738;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region E109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=78158406; PubMed=417344;
RX Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
RL Proc Natl Acad Sci U S A. 75:1957-1961(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; C93818; AVMS09.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SMC0406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113
SQ SEQUENCE 113 AA; 12647 MW; E50F2F20EDB129B CRC64;

Query Match 10.4%; Score 12; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 6 ESGGGLVQPGGS 17

RESULT 12
HV30 MOUSE
ID HV30 MOUSE STANDARD; PRT; 113 AA.
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region ABE-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=77134726; PubMed=402936;
RX Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
proteins.";
RL Biochemistry 16:1170-1175(1977).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90400; AVMSB7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SMC0406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 10.4%; Score 12; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 6 ESGGGLVQPGGS 17

RESULT 13
HV31 MOUSE
ID HV31 MOUSE STANDARD; PRT; 113 AA.
AC P01800;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region T957.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=81216632; PubMed=6787122;
RX Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A92810; AVMS57.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SMC0406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 113
SQ SEQUENCE 113 AA; 12732 MW; 26618F626B59859E CRC64;

Query Match 10.4%; Score 12; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
DB 6 ESGGGLVQPGGS 17

RESULT 14
HV32 MOUSE
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ID HV32_MOUSE STANDARD; PRT; 115 AA.
AC P01801;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; C92811; AVMS06.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 114 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; B67AD6638A121A5P CRC64;

Query Match 10.4%; Score 12; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
Db 6 ESGGGLVQPGGS 17

RESULT 15
HV33_MOUSE STANDARD; PRT; 115 AA.
ID HV33_MOUSE
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; D92811; AVMS82.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 114 IG-LIKE.

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FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Query Match 10.4%; Score 12; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ESGGGLVQPGGS 17
Db 6 ESGGGLVQPGGS 17

RESULT 16
HV34_MOUSE STANDARD; PRT; 113 AA.
ID HV34_MOUSE
AC P01803;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region AMPCL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
RT evidence for a new heavy chain joining segment.";
RL J. Immunol. 127:191-194(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02073; HVMSAW.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >113 IG-LIKE.
FT DISULFID 22 98 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12691 MW; 7A6D906AAA966E9E CRC64;

Query Match 9.6%; Score 11; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 SVKGRFTISR 73
Db 65 SVKGRFTISR 75

RESULT 17
HV47_MOUSE STANDARD; PRT; 113 AA.
ID HV47_MOUSE
AC P01823;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-60.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84024551; PubMed=6414509;

```

RA Juszczak E.C., Margolies M.N.;  
 RT "Amino acid sequence of the heavy chain variable region from the A/J  
 mouse anti-arsenate monoclonal antibody 36-60 bearing a minor  
 idiotype.";  
 RL Biochemistry 22:4291-4296(1983).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE  
 MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND  
 CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF  
 CC STRAIN A/J MICE.  
 CC PIR; A02098; G2MS60.  
 DR PDB; 1J1P; 18-FEB-03.  
 DR PDB; 1J1P; 18-FEB-03.  
 DR PDB; 1J1X; 18-FEB-03.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS08335; IG-LIKE; 1.  
 DR Immunoglobulin V region; 3D-structure.  
 FT NON TER 113 114  
 SQ SEQUENCE 113 AA; 12734 MW; 38DC0E0B3F5075B7 CRC64;  
 Query Match 6.1%; Score 7; DB 1; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VOLQESG 8  
 DB 2 VOLQESG 8  
 RESULT 18  
 HV00 MOUSE  
 ID HV00 MOUSE STANDARD; PRT; 114 AA.  
 AC P01741;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region (Anti-arsenate antibody).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=A/J;  
 RX MEDLINE=79195438; PubMed=109536;  
 RA Capra J.D.; Nisonoff A.;  
 RT "Structural studies on induced antibodies with defined idiotypic  
 specificity. VII. The complete amino acid sequence of the heavy  
 chain variable region of anti-p-azophenylarsenate antibodies from A/J  
 mice bearing a cross-reactive idiotype.";  
 RL J. Immunol. 123:279-284(1979).  
 CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF  
 THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V  
 REGION SEQUENCE.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02022; G1MSAA.  
 DR HSP; P01772; 2FB4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS08335; IG-LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 106  
 NON TER 114 114  
 SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A59F4BE CRC64;  
 Query Match 6.1%; Score 7; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPG 42  
 DB 36 WVRQAPG 42  
 RESULT 19  
 HV2A RABIT  
 ID HV2A RABIT STANDARD; PRT; 114 AA.  
 AC P01827;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-A2 region BS-1.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76277871; PubMed=9073;  
 RA Jaton J.-C.;  
 RT "The V-region sequence of the H chain from a third rabbit anti-  
 pneumococcal antibody.";  
 RL Biochem. J. 157:449-459(1976).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III  
 PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02103; GARB21.  
 DR HSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS08335; IG-LIKE; 1.  
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.  
 FT DOMAIN 1 107  
 NON TER 114 114  
 SQ SEQUENCE 114 AA; 12325 MW; 466F5EE1E55C1F96 CRC64;  
 Query Match 6.1%; Score 7; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 WVRQAPG 42  
 DB 36 WVRQAPG 41  
 RESULT 20  
 HV44 MOUSE  
 ID HV44 MOUSE STANDARD; PRT; 115 AA.  
 AC P01820;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region PUL4 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81012133; PubMed=6774258;  
 RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;  
 RT "Two types of somatic recombination are necessary for the generation  
 of complete immunoglobulin heavy-chain genes.";  
 RL Nature 286:676-683(1980).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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EMBL; V00767; CRA24148.1; -;  
DR PIR; A02095; HVM514.  
DR PDB; 1A7N; 29-APR-98.  
DR PDB; 1A7O; 29-APR-98.  
DR PDB; 1A7P; 29-APR-98.  
DR PDB; 1A7R; 29-APR-98.  
DR PDB; 1G7H; 17-JAN-01.  
DR PDB; 1G7I; 17-JAN-01.  
DR PDB; 1G7J; 17-JAN-01.  
DR PDB; 1G7M; 17-JAN-01.  
DR PDB; 43C9; 24-JUL-02.  
DR PDB; 43CA; 24-JUL-02.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal; 3D-structure.  
FT SIGNAL 19  
FT CHAIN 20 115 IG HEAVY CHAIN V REGION PJ14.  
FT DOMAIN 20 >115 IG-LIKE.  
FT NON\_TER 115  
SQ SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;

Query Match 6.1%; Score 7; DB 1; Length 115;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 PGKLEW 47  
DB 60 PGKLEW 66

RESULT 21  
YVED\_VACC STANDARD; PRT; 66 AA.  
AC P20556;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 7.6 kDa protein.  
E ORF D.  
OS Vaccinia virus (strain Copenhagen).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10249;  
RN [1]  
RP MEDLINE=91021027; PubMed=2219722;  
RX Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
FAoletti E.;  
RT "The complete DNA sequence of vaccinia virus."  
RL Virology 179:247-266(1990).  
RN [2]  
RP COMPLETE GENOME.  
RX Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,  
FAoletti E.;  
RT "Appendix to 'The complete DNA sequence of vaccinia virus'";  
RL Virology 179:517-563(1990).

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DR EMBL; M35027; AAA48048.1; -;  
DR PIR; A42510; A42510.  
KW Hypothetical protein.  
SQ SEQUENCE 66 AA; 7645 MW; 0D57ED3FB0880C17 CRC64;

Query Match 5.2%; Score 6; DB 1; Length 66;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 FTFSSY 32  
DB 38 FTFSSY 43

## RESULT 22

RPOZ\_BACSU STANDARD; PRT; 67 AA.

AC Q35011;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Probable DNA-directed RNA polymerase omega chain (EC 2.7.7.6)  
DE (Transcriptase omega chain) (RNA polymerase omega subunit).  
GN RPOZ OR BSU15690.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=98195738; PubMed=9534248;  
RA Foulger D., Errington J.;  
RT "A 28 kbp segment from the spoVM region of the Bacillus subtilis 168  
genome".  
RL Microbiology 144:801-805(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=98044033; PubMed=9384377;  
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
RA Azevedo V., Betero M.G., Bessieres P., Bolotin A., Borchert S.,  
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
RA Entiaz K.D., Errington J., Fabret C., Ferrati E., Foulger D.,  
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
RA Giuseppe H., Guy B.J., Haga K., Haeck J., Harwood C.R., Henaut A.,  
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,  
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
RA Parro V., Portetle D., Portetle D., Porwollik S., Prescott A.M.,  
RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
RA Rieger M., Rivolta C., Rocha E., Roche M., Rose M., Sadale Y.,  
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
RA Sakiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,  
RA Srokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
RA Takeuchi M., Tanakoshi A., Tanaka T., Terstra P., Tognoni A.,  
RA Tsutao T., Uchiyama S., Vandenbol M., Vanlier F., Vassarotti A.,  
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;  
RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
subtilis".  
RL Nature 390:249-256(1997).

CC -!- FUNCTION: Promotes RNA polymerase assembly. Latches the N- and C-  
CC terminal regions of the beta' subunit thereby facilitating its  
CC interaction with the beta and alpha subunits (By similarity).  
CC



CC -|- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
CC [RNA] (N).  
CC -|- SUBUNIT: Consists of a sigma factor and the RNAP core enzyme which  
CC is composed of 2 alpha chains, 1 beta chain, 1 beta' chain and 1  
CC omega chain (By similarity).  
CC -|- SIMILARITY: Belongs to the RNA polymerase omega chain family.  
CC  
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CC  
CC EMBL; Y13937; CA474272.1; -;  
CC EMBL; Z99112; CAB13442.1; -;  
CC PIR; C69878; C69878.  
CC HAMAP; MF\_00366; -; 1.  
CC InterPro; IPR003716; RNA\_pol\_omega.  
CC InterPro; IPR006110; RNA\_pol\_Rpb6.  
CC Pfam; PF01192; RNA\_pol\_Rpb6; 1.  
CC TIGRFAMs; TIGR00690; rpoZ; 1.  
KW Transferase; DNA-directed RNA polymerase; Transcription;  
KW Complete proteome.  
SQ SEQUENCE 67 AA; 7754 MW; 022B8C8A5E371409 CRC64;  
  
Query Match 5.2%; Score 6; DB 1; Length 67;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 109 TLTVTS 114  
Db 18 TLTVTS 23  
|||||  
18 TLTVTS 23  
  
RESULT 23  
RPOZ BACHD STANDARD; PRT; 68 AA.  
ID RPOZ BACHD  
AC Q9K9Y3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Probable DNA-directed RNA polymerase omega chain (EC 2.7.7.6)  
DE (Transcriptase omega chain) (RNA polymerase omega subunit).  
GN RPOZ OR BH2511.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RA MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fuji F., Hirata C., Nakamura Y., Ogasawara N., Kuhara S.,  
RA Horikoshi K.  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans and genomic sequence comparison with Bacillus subtilis."  
RL Nucleic Acids Res. 28:4317-4331(2000).  
CC -|- FUNCTION: Promotes RNA polymerase assembly. Latches the N- and C-  
CC terminal regions of the beta' subunit thereby facilitating its  
CC interaction with the beta and alpha subunits (By similarity).  
CC -|- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
CC [RNA] (N).  
CC -|- SUBUNIT: Consists of a sigma factor and the RNAP core enzyme which  
CC is composed of 2 alpha chains, 1 beta chain, 1 beta' chain and 1  
CC omega chain (By similarity).  
CC -|- SIMILARITY: Belongs to the RNA polymerase omega chain family.  
CC  
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CC  
CC EMBL; AP001515; BAB06230.1; -;  
CC PIR; G83963; G83963.  
CC HAMAP; MF\_00366; -; 1.  
CC InterPro; IPR003716; RNA\_pol\_omega.  
CC InterPro; IPR006110; RNA\_pol\_Rpb6.  
CC Pfam; PF01192; RNA\_pol\_Rpb6; 1.  
CC TIGRFAMs; TIGR00690; rpoZ; 1.  
KW Transferase; DNA-directed RNA polymerase; Transcription;  
KW Complete proteome.  
SQ SEQUENCE 68 AA; 7820 MW; E0279B9CED016500 CRC64;  
  
Query Match 5.2%; Score 6; DB 1; Length 68;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 109 TLTVTS 114  
Db 18 TLTVTS 23  
|||||  
18 TLTVTS 23  
  
RESULT 24  
NEUL STRCA STANDARD; PRT; 93 AA.  
ID NEUL STRCA  
AC P15444;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neurophysin 1.  
OS Struthio camelus (Ostrich).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;  
OC Struthio.  
OX NCBI\_TaxID=8801;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=88138569; PubMed=3436699;  
RA Lazure C., Saayman H.S., Naude R.J., Oelofsen W., Chretien M.;  
RT "Complete amino acid sequence of a VLDV-type neurophysin from ostrich  
RT differs markedly from known mammalian neurophysins.";  
RL Int. J. Pept. Protein Res. 30:634-645(1987).  
CC -|- FUNCTION: NEUROPHYSIN 1 SPECIFICALLY BINDS OXYTOCIN.  
CC -|- SIMILARITY: Belongs to the vasopressin/oxytocin family.  
CC PIR; J50301; J50301.  
CC HSSP; P01180; 2BN2.  
CC InterPro; IPR00981; Neurhyp\_horm.  
CC Pfam; PF00184; hormones; 1.  
CC PRINTS; PR00831; NEUROPHYSIN.  
CC ProDom; PD001676; Neurhyp\_horm; 1.  
CC SMART; SM00003; NH; 1.  
FT DISULFID 10 54 BY SIMILARITY.  
FT DISULFID 13 27 BY SIMILARITY.  
FT DISULFID 28 34 BY SIMILARITY.  
FT DISULFID 21 44 BY SIMILARITY.  
FT DISULFID 61 74 BY SIMILARITY.  
FT DISULFID 68 86 BY SIMILARITY.  
FT DISULFID 75 80 BY SIMILARITY.  
SQ SEQUENCE 93 AA; 9971 MW; 7C8A9FBE2AC1444 CRC64;  
  
Query Match 5.2%; Score 6; DB 1; Length 93;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 21 SCAASG 26  
Db 67 SCAASG 72  
|||||  
67 SCAASG 72  
  
RESULT 25

Mon Mar 15 09:47:37 2004

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YG81_WOLSU
ID_YG81_WOLSU STANDARD; PRT; 102 AA.
AC O34247;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical UPF0133 protein WS1681.
GN WS1681.
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSMZ 1740;
RX MEDLINE=98305043; PubMed=9639603;
RA Gross R., Simon J., Theis F., Kroeger A.;
RT "Two membrane anchors of Wolinella succinogenes hydrogenase and their
RL function in fumarate and polysulfide respiration.";
RN Arch. Microbiol. 170:50-58(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DSMZ 1740;
RX MEDLINE=22882897; PubMed=14500908;
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer F., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the UPF0133 family.
CC -----
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CC -----
DR EMBL; AJ003049; CAA05823.1; -.
DR EMBL; BX571661; CAE10708.1; ALT_INIT.
DR HAMAP; MF 00274; -.
DR InterPro; IPR004401; Cons_hypoth103.
DR Pfam; PF02575; DUF149; 1.
DR TIGRFAMs; TIGR00103; TIGR00103; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 102 AA; 10997 MW; B50D321F69AB63A2 CRC64;

Query Match 5.2%; Score 6; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGGGLV 12
DB 34 SGGGLV 39

Search completed: March 15, 2004, 07:37:07
Job time : 21 secs

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